

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2005, 17:23:48 ; Search time 62 Seconds  
(without alignments)  
1338.972 Million cell updates/sec

Perfect score: 1102

Sequence: 1 MLMLFLVTAIHAELCPG.....ENGIRSDPLDMKGILMPS 212

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US10G\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep:\*

21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	1102	100.0	212	10	US-09-997-482-487
515	1102	100.0	212	17	US-10-931-886-482
517	1102	100.0	212	18	US-10-935-952-482
518	1073	97.4	222	14	US-10-097-065-141
519	1073	97.4	222	15	US-10-372-876-141
520	1066	96.7	222	10	US-09-948-783-129
521	1066	96.7	223	10	US-09-892-877-128
522	663	60.2	176	14	US-10-097-065-274
523	663	60.2	176	15	US-10-372-876-274
524	415	37.7	105	14	US-10-097-065-246
525	415	37.7	105	15	US-10-372-876-246
526	376	34.1	805	9	US-09-978-385-2

527	376	34.1	805	11	US-09-999-781-2	Sequence 2, App1
528	376	34.1	805	13	US-10-114-893-86	Sequence 86, App1
529	376	34.1	805	14	US-10-158-847-142	Sequence 142, App
530	376	34.1	805	14	US-10-005-956-570	Sequence 570, App
531	376	34.1	805	14	US-10-005-956-843	Sequence 843, App
532	376	34.1	805	14	US-10-158-825-142	Sequence 142, App
533	376	34.1	805	16	US-10-158-825-142	Sequence 142, App
534	376	34.1	805	20	US-11-059-218-2	Sequence 2, App1
535	376	34.1	805	20	US-11-059-218-106	Sequence 106, App
536	361	32.8	805	9	US-09-978-385-6	Sequence 6, App1
537	361	32.8	805	9	US-09-978-385-9	Sequence 9, App1
538	359	32.6	711	9	US-09-969-384-13	Sequence 13, App1
539	359	32.6	711	14	US-10-158-847-138	Sequence 138, App
540	359	32.6	711	14	US-10-158-825-138	Sequence 138, App
541	359	32.6	711	16	US-10-158-825-138	Sequence 138, App
542	359	32.6	64	9	US-09-864-761-35999	Sequence 35999, A
543	289	26.2	681	9	US-09-969-384-25	Sequence 25, App1
544	289	26.2	681	14	US-10-158-847-140	Sequence 140, App
545	289	26.2	681	14	US-10-158-825-140	Sequence 140, App
546	289	26.2	681	16	US-10-158-825-140	Sequence 140, App
547	133	12.1	24	14	US-10-097-065-277	Sequence 277, App
548	133	12.1	24	15	US-10-372-876-277	Sequence 277, App
549	117	10.6	23	14	US-10-097-065-276	Sequence 276, App
550	117	10.6	23	15	US-10-372-876-276	Sequence 276, App
551	91.5	8.3	545	10	US-09-866-050A-500	Sequence 500, App
552	91.5	8.3	688	10	US-09-866-050A-624	Sequence 624, App
553	90	8.2	25	14	US-10-097-065-275	Sequence 275, App
554	90	8.2	25	15	US-10-372-876-275	Sequence 275, App
555	89.5	8.1	1063	15	US-10-161-493-66	Sequence 66, App1
556	89	8.1	799	14	US-10-174-677-26	Sequence 26, App1
557	89	8.1	799	16	US-10-678-160A-3	Sequence 3, App1
558	88.5	8.0	1063	15	US-10-161-493-64	Sequence 64, App1
559	88	8.0	365	9	US-09-870-755-73	Sequence 73, App1
560	88	8.0	365	10	US-09-751-708A-73	Sequence 73, App1
561	88	8.0	365	16	US-10-428-817A-69	Sequence 69, App1
562	88	8.0	365	17	US-10-937-758A-50	Sequence 50, App1
563	86.5	7.8	887	16	US-10-425-115A-227399	Sequence 327399, A
564	86	7.8	364	18	US-10-024-607-8	Sequence 8, App1
565	85.5	7.8	545	14	US-10-243-243A-4	Sequence 4, App1
566	85.5	7.8	583	14	US-10-142-515-4	Sequence 4, App1
567	85.5	7.8	959	10	US-09-894-159-33	Sequence 33, App1
568	85.5	7.8	959	10	US-09-894-159-93	Sequence 93, App1
569	85.5	7.8	1148	9	US-09-884-441-478	Sequence 478, App
570	85.5	7.8	1148	9	US-09-884-441-459	Sequence 459, App
571	85.5	7.8	1148	10	US-09-907-969-458	Sequence 458, App
572	85.5	7.8	1148	10	US-09-907-969-479	Sequence 479, App
573	85.5	7.8	1148	10	US-09-827-271-458	Sequence 458, App
574	85.5	7.8	1148	14	US-10-097-340-216	Sequence 216, App
575	85.5	7.8	1148	14	US-10-198-053-458	Sequence 458, App
576	85.5	7.8	1148	14	US-10-198-053-479	Sequence 479, App
577	85.5	7.8	1148	15	US-10-257-021-56	Sequence 56, App1
578	85.5	7.8	1148	15	US-10-383-388-2	Sequence 2, App1
579	85.5	7.8	1148	16	US-10-734-564-131	Sequence 131, App
580	85.5	7.8	1148	17	US-10-860-790-458	Sequence 458, App
581	85.5	7.8	1148	17	US-10-860-790-479	Sequence 479, App
582	85.5	7.8	1148	17	US-10-936-626-129	Sequence 129, App
583	85.5	7.8	1148	17	US-10-938-061-129	Sequence 129, App
584	85.5	7.8	1156	9	US-09-884-441-459	Sequence 459, App
585	85.5	7.8	1156	9	US-09-907-969-459	Sequence 459, App
586	85.5	7.8	1156	10	US-09-827-271-459	Sequence 459, App
587	85.5	7.8	1156	14	US-10-198-053-459	Sequence 459, App
588	85.5	7.8	1156	17	US-10-860-790-459	Sequence 459, App
589	85.5	7.8	1156	17	US-10-860-790-459	Sequence 459, App
590	85	7.7	1337	15	US-10-142-515-5	Sequence 5, App1
591	84.5	7.7	1337	15	US-10-366-547-84	Sequence 84, App1
592	84.5	7.7	1337	15	US-10-291-634-3	Sequence 3, App1
593	84.5	7.7	1188	15	US-10-291-265-338	Sequence 338, App
594	83.5	7.6	1337	14	US-10-390-501-2	Sequence 2, App1
595	83.5	7.6	1337	15	US-10-366-547-42	Sequence 42, App1
596	83.5	7.6	1337	16	US-10-723-606-2	Sequence 2, App1
597	82.5	7.5	809	17	US-10-687-035-2	Sequence 2, App1
598	82	7.4	1120	15	US-10-262-839-6	Sequence 6, App1
599	82	7.4	1189	10	US-09-984-130-35	Sequence 35, App1

600	82	7.4	1189	10	US-09-836-353A-35	Sequence 35, App1	673	78.5	7.1	914	17	US-10-860-790-478	Sequence 478, App
601	82	7.4	1189	15	US-10-262-839-4	Sequence 478, App1	674	78.5	7.1	2127	16	US-10-437-963-198585	Sequence 198585, App
602	82	7.4	1189	16	US-10-723-860-2788	Sequence 2788, App	675	78.5	7.1	3451	10	US-09-907-969-599	Sequence 595, App
603	82	7.4	1216	15	US-10-366-547-49	Sequence 49, App1	676	78.5	7.1	3451	14	US-10-198-053-595	Sequence 595, App
604	81.5	7.4	302	14	US-10-032-214-268	Sequence 268, App	677	78.5	7.1	3451	17	US-10-860-790-595	Sequence 595, App
605	81.5	7.4	302	18	US-10-479-501-268	Sequence 268, App	678	78.5	7.1	300	14	US-10-032-214-196	Sequence 196, App
606	81.5	7.4	1048	10	US-09-920-267C-9	Sequence 9, App1	679	78	7.1	300	18	US-10-479-901-196	Sequence 196, App
607	81.5	7.4	1048	15	US-10-211-462-189	Sequence 9, App1	680	78	7.1	300	9	US-09-985-694A-9	Sequence 9, App1
608	81.5	7.4	1048	16	US-10-720-323-3	Sequence 9, App1	681	78	7.1	343	10	US-09-929-752-9	Sequence 9, App1
609	81.5	7.4	1048	16	US-10-769-565-9	Sequence 9, App1	682	78	7.1	343	13	US-10-176-079-9	Sequence 9, App1
610	81.5	7.4	1048	16	US-10-484-568-75	Sequence 75, App1	683	78	7.1	343	14	US-10-184-426-9	Sequence 9, App1
611	81.5	7.4	1048	17	US-10-482-029-20	Sequence 20, App1	684	78	7.1	343	14	US-10-305-555-14	Sequence 14, App1
612	81	7.4	1135	11	US-09-972-211-108	Sequence 108, App	685	78	7.1	354	17	US-10-485-555-58	Sequence 58, App1
613	81	7.4	1135	15	US-10-096-625-108	Sequence 108, App	686	78	7.1	555	14	US-10-288-252-9	Sequence 9, App1
614	81	7.4	1179	11	US-09-972-211-109	Sequence 109, App	687	78	7.1	555	16	US-10-398-038-9	Sequence 9, App1
615	81	7.4	1179	15	US-10-096-625-109	Sequence 109, App	688	78	7.1	555	17	US-10-976-440-9	Sequence 9, App1
616	80.5	7.3	284	10	US-09-965-738-100	Sequence 100, App	689	78	7.1	887	14	US-10-132-350-18	Sequence 18, App1
617	80.5	7.3	430	16	US-10-437-963-198596	Sequence 198596, App	690	78	7.1	887	14	US-10-132-350-20	Sequence 20, App1
618	80.5	7.3	438	9	US-09-884-441-483	Sequence 483, App	691	78	7.1	926	15	US-10-425-114-69756	Sequence 69756, A
619	80.5	7.3	438	10	US-09-907-969-483	Sequence 483, App	692	77.5	7.0	232	17	US-10-495-148-33	Sequence 33, App1
620	80.5	7.3	438	14	US-10-198-053-483	Sequence 483, App	693	77.5	7.0	330	16	US-10-437-963-120185	Sequence 120185, App1
621	80.5	7.3	438	15	US-10-333-900-19	Sequence 19, App1	694	77	7.0	661	16	US-10-437-963-183011	Sequence 183011, App1
622	80.5	7.3	438	17	US-10-860-790-483	Sequence 483, App	695	76.5	6.9	303	14	US-10-032-214-59	Sequence 59, App1
623	80.5	7.3	439	10	US-09-965-738-148	Sequence 148, App	696	76.5	6.9	303	18	US-10-479-901-59	Sequence 59, App1
624	80.5	7.3	526	15	US-10-333-900-30	Sequence 30, App1	697	76.5	6.9	314	14	US-10-032-585-7686	Sequence 7686, App
625	80.5	7.3	1148	10	US-09-932-419-2	Sequence 2, App1	698	76.5	6.9	542	10	US-09-972-268-4	Sequence 2, App1
626	80.5	7.3	1148	10	US-09-965-738-48	Sequence 48, App1	699	76.5	6.9	549	10	US-09-972-268-2	Sequence 4, App1
627	80.5	7.3	2248	10	US-09-965-738-50	Sequence 50, App1	700	76.5	6.9	549	10	US-09-972-268-6	Sequence 6, App1
628	80.5	7.3	11721	10	US-09-965-738-162	Sequence 162, App1	701	76.5	6.9	549	14	US-10-161-572-45	Sequence 45, App1
629	80.5	7.3	22152	16	US-10-715-066-5	Sequence 5, App1	702	76.5	6.9	666	15	US-10-424-599-195355	Sequence 195355, App1
630	79.5	7.2	340	15	US-10-051-874-78	Sequence 78, App1	703	76.5	6.9	794	15	US-10-072-012-484	Sequence 84, App
631	79.5	7.2	355	15	US-10-369-493-345	Sequence 345, App	704	76	6.9	199	14	US-10-021-660-82	Sequence 82, App1
632	79.5	7.2	502	14	US-10-156-761-11794	Sequence 11794, A	705	76	6.9	230	16	US-10-408-765-3366	Sequence 356, App
633	79.5	7.2	1890	14	US-10-097-340-217	Sequence 217, App	706	76	6.9	820	16	US-10-437-963-131866	Sequence 131866, App
634	79.5	7.2	1890	15	US-10-245-871-314	Sequence 314, App	707	76	6.9	906	16	US-10-437-963-131866	Sequence 131866, App
635	79.5	7.2	1890	15	US-10-253-286-314	Sequence 314, App	708	75.5	6.9	127	15	US-10-264-237-1908	Sequence 1908, App
636	79.5	7.2	2234	15	US-10-612-090-20	Sequence 20, App1	709	75.5	6.9	133	9	US-09-864-761-35106	Sequence 35106, A
637	79	7.2	2029	15	US-10-087-684-38	Sequence 38, App1	710	75.5	6.9	249	15	US-10-417-312-8	Sequence 8, App1
638	79	7.2	2029	15	US-10-087-684-38	Sequence 38, App1	711	75.5	6.9	249	15	US-10-417-312-9	Sequence 9, App1
639	79	7.2	2037	15	US-10-087-684-39	Sequence 39, App1	712	75.5	6.9	255	15	US-10-417-312-6	Sequence 6, App1
640	79	7.2	2037	15	US-10-218-779-39	Sequence 39, App1	713	75.5	6.9	264	15	US-10-417-312-7	Sequence 7, App1
641	78.5	7.1	233	9	US-09-884-441-488	Sequence 488, App	714	75.5	6.9	264	15	US-10-447-839-105	Sequence 105, App
642	78.5	7.1	233	10	US-09-907-969-488	Sequence 488, App	715	75.5	6.9	273	15	US-10-417-312-4	Sequence 4, App1
643	78.5	7.1	233	14	US-10-198-053-488	Sequence 488, App	716	75.5	6.9	282	15	US-10-417-312-5	Sequence 5, App1
644	78.5	7.1	233	17	US-10-860-790-488	Sequence 488, App	717	75.5	6.9	299	14	US-10-032-214-481	Sequence 49, App1
645	78.5	7.1	306	16	US-10-425-115-195472	Sequence 195472, App	718	75.5	6.9	299	14	US-10-032-214-289	Sequence 289, App1
646	78.5	7.1	318	10	US-09-907-969-594	Sequence 594, App	719	75.5	6.9	299	18	US-10-479-901-49	Sequence 49, App1
647	78.5	7.1	318	14	US-10-198-053-594	Sequence 594, App	720	75.5	6.9	299	18	US-10-479-901-281	Sequence 281, App
648	78.5	7.1	318	17	US-10-860-790-594	Sequence 594, App	721	75.5	6.9	301	14	US-10-032-214-192	Sequence 192, App
649	78.5	7.1	438	9	US-09-884-441-390	Sequence 390, App	722	75.5	6.9	301	14	US-10-479-901-192	Sequence 192, App
650	78.5	7.1	438	10	US-09-907-969-390	Sequence 390, App	723	75.5	6.9	302	14	US-10-032-214-62	Sequence 62, App1
651	78.5	7.1	438	10	US-09-827-271-390	Sequence 390, App	724	75.5	6.9	302	14	US-10-032-214-180	Sequence 180, App
652	78.5	7.1	438	14	US-10-198-053-390	Sequence 390, App	725	75.5	6.9	302	14	US-10-032-214-195	Sequence 195, App
653	78.5	7.1	438	17	US-10-860-790-390	Sequence 390, App	726	75.5	6.9	302	14	US-10-032-214-203	Sequence 203, App
654	78.5	7.1	696	10	US-09-866-050A-501	Sequence 501, App	727	75.5	6.9	302	14	US-10-032-214-213	Sequence 213, App
655	78.5	7.1	833	9	US-09-884-441-389	Sequence 389, App	728	75.5	6.9	302	14	US-10-032-214-219	Sequence 219, App
656	78.5	7.1	833	10	US-09-907-969-389	Sequence 389, App	729	75.5	6.9	302	18	US-10-479-901-62	Sequence 62, App1
657	78.5	7.1	833	10	US-09-827-271-389	Sequence 389, App	730	75.5	6.9	302	18	US-10-479-901-180	Sequence 180, App
658	78.5	7.1	833	14	US-10-198-053-389	Sequence 389, App	731	75.5	6.9	302	18	US-10-479-901-195	Sequence 195, App
659	78.5	7.1	833	17	US-10-860-790-389	Sequence 389, App	732	75.5	6.9	302	18	US-10-479-901-203	Sequence 203, App
660	78.5	7.1	914	9	US-09-778-320-206	Sequence 206, App	733	75.5	6.9	302	18	US-10-479-901-213	Sequence 213, App
661	78.5	7.1	914	9	US-09-910-689-206	Sequence 206, App	734	75.5	6.9	302	18	US-10-479-901-219	Sequence 219, App
662	78.5	7.1	914	9	US-09-884-441-312	Sequence 312, App	735	75.5	6.9	303	14	US-10-032-214-204	Sequence 204, App
663	78.5	7.1	914	10	US-09-884-441-478	Sequence 478, App	736	75.5	6.9	303	14	US-10-032-214-211	Sequence 211, App
664	78.5	7.1	914	10	US-09-907-969-312	Sequence 312, App	737	75.5	6.9	303	18	US-10-479-901-204	Sequence 204, App
665	78.5	7.1	914	10	US-09-907-969-478	Sequence 478, App	738	75.5	6.9	303	18	US-10-479-901-211	Sequence 211, App
666	78.5	7.1	914	10	US-09-827-271-312	Sequence 312, App	739	75.5	6.9	312	15	US-10-296-734-824	Sequence 824, App
667	78.5	7.1	914	13	US-10-010-742-206	Sequence 206, App	740	75.5	6.9	321	9	US-09-925-301-861	Sequence 861, App
668	78.5	7.1	914	14	US-10-198-053-312	Sequence 312, App	741	75.5	6.9	475	15	US-10-417-312-1-9	Sequence 1, App1
669	78.5	7.1	914	14	US-10-198-053-478	Sequence 478, App	742	75.5	6.9	475	17	US-10-696-633-59	Sequence 59, App1
670	78.5	7.1	914	16	US-10-714-389-206	Sequence 206, App	743	75.5	6.9	475	20	US-11-055-119-67	Sequence 67, App1
671	78.5	7.1	914	16	US-10-717-296-206	Sequence 206, App	744	75.5	6.9	495	20	US-11-055-119-67	Sequence 67, App1
672	78.5	7.1	914	17	US-10-860-790-312	Sequence 312, App	745	75.5	6.9	515	14	US-10-097-340-212	Sequence 212, App

746	75.5	6.9	515	14	US-10-171-311-156	Sequence 156, App	819	72.5	6.6	231	15	US-10-369-493-5603	Sequence 5603, App
747	75.5	6.9	515	15	US-10-612-090-19	Sequence 19, App	820	72.5	6.6	252	17	US-10-794-514A-440	Sequence 440, App
748	75.5	6.9	549	15	US-10-282-122A-42803	Sequence 42803, A	821	72.5	6.6	302	14	US-10-032-214-272	Sequence 272, App
749	75.5	6.9	1255	10	US-09-966-069-10	Sequence 10, App	822	72.5	6.6	302	18	US-10-479-901-272	Sequence 272, App
750	75.5	6.9	1255	14	US-10-171-311-158	Sequence 158, App	823	72.5	6.6	303	14	US-10-032-214-61	Sequence 61, App
751	75.5	6.9	1255	14	US-10-177-293-311	Sequence 311, App	824	72.5	6.6	303	14	US-10-032-214-185	Sequence 185, App
752	75.5	6.9	1255	16	US-10-734-564-120	Sequence 120, App	825	72.5	6.6	303	14	US-10-032-214-193	Sequence 193, App
753	75.5	6.9	1255	17	US-10-473-484-2	Sequence 2, App	826	72.5	6.6	303	14	US-10-032-214-193	Sequence 193, App
754	75.5	6.9	1713	14	US-10-270-333-177	Sequence 177, App	827	72.5	6.6	303	14	US-10-032-214-193	Sequence 193, App
755	75	6.8	92	18	US-10-425-115-263281	Sequence 263281, App	828	72.5	6.6	303	14	US-10-032-214-183	Sequence 283, App
756	75	6.8	548	16	US-10-724-972A-7488	Sequence 7488, App	829	72.5	6.6	303	18	US-10-479-901-61	Sequence 61, App
757	75	6.8	1260	9	US-09-893-238-2	Sequence 2, App	830	72.5	6.6	303	18	US-10-479-901-185	Sequence 185, App
758	75	6.8	1428	11	US-09-964-956-34	Sequence 34, App	831	72.5	6.6	303	18	US-10-479-901-186	Sequence 186, App
759	74.5	6.8	204	16	US-10-477-527-23	Sequence 23, App	832	72.5	6.6	303	18	US-10-479-901-193	Sequence 193, App
760	74.5	6.8	213	16	US-10-425-115-311769	Sequence 311769, App	833	72.5	6.6	303	18	US-10-479-901-197	Sequence 197, App
761	74.5	6.8	307	9	US-09-825-882-18	Sequence 18, App	834	72.5	6.6	303	18	US-10-479-901-283	Sequence 283, App
762	74.5	6.8	307	14	US-10-017-161-1786	Sequence 1786, App	835	72.5	6.6	393	16	US-10-417-315-145	Sequence 145, App
763	74.5	6.8	307	15	US-10-293-798-1442	Sequence 1442, App	836	72.5	6.6	641	15	US-10-257-384A-2	Sequence 2, App
764	74.5	6.8	307	15	US-10-343-650A-680	Sequence 680, App	837	72.5	6.6	650	15	US-10-424-599-226788	Sequence 226788, App
765	74.5	6.8	307	16	US-10-724-208-18	Sequence 18, App	838	72.5	6.6	157	11	US-09-833-245-2061	Sequence 2061, App
766	74.5	6.8	307	16	US-10-770-127-189	Sequence 189, App	839	72	6.5	157	14	US-10-060-255-54	Sequence 54, App
767	74.5	6.8	307	16	US-10-724-209-18	Sequence 18, App	840	72	6.5	185	16	US-10-881-088-54	Sequence 54, App
768	74.5	6.8	307	17	US-10-986-871-18	Sequence 18, App	841	72	6.5	185	16	US-10-060-255-77	Sequence 77, App
769	74	6.7	589	15	US-10-369-493-23314	Sequence 23314, A	842	72	6.5	185	16	US-10-881-088-77	Sequence 77, App
770	74	6.7	679	16	US-10-425-115-251049	Sequence 251049, A	843	72	6.5	266	15	US-10-424-599-237242	Sequence 237242, App
771	74	6.7	701	15	US-10-425-114-72520	Sequence 72520, A	844	72	6.5	323	9	US-09-815-087-4	Sequence 4, App
772	73.5	6.7	299	14	US-10-032-214-50	Sequence 50, App	845	72	6.5	323	14	US-10-266-643-4	Sequence 4, App
773	73.5	6.7	299	18	US-10-479-901-50	Sequence 50, App	846	72	6.5	453	16	US-10-437-963-128099	Sequence 128099, App
774	73.5	6.7	303	14	US-10-032-214-188	Sequence 188, App	847	72	6.5	526	14	US-10-021-425-27	Sequence 27, App
775	73.5	6.7	303	14	US-10-032-214-200	Sequence 200, App	848	72	6.5	526	17	US-10-900-856-10	Sequence 30, App
776	73.5	6.7	303	14	US-10-032-214-201	Sequence 201, App	849	72	6.5	792	15	US-10-072-012-483	Sequence 483, App
777	73.5	6.7	303	18	US-10-479-901-188	Sequence 188, App	850	72	6.5	865	16	US-10-437-963-165232	Sequence 203508, App
778	73.5	6.7	303	18	US-10-479-901-200	Sequence 200, App	851	72	6.5	888	16	US-10-437-963-15789	Sequence 15789, App
779	73.5	6.7	303	18	US-10-479-901-201	Sequence 201, App	852	72	6.5	1447	15	US-10-425-114-57769	Sequence 57769, A
780	73.5	6.7	442	15	US-10-424-599-243138	Sequence 243138, App	853	72	6.5	1505	15	US-10-369-493-984	Sequence 4984, App
781	73.5	6.7	498	15	US-10-369-493-6826	Sequence 6826, App	854	72	6.5	2105	15	US-10-282-122A-76671	Sequence 76871, A
782	73.5	6.7	498	15	US-10-369-493-6826	Sequence 6826, App	855	71.5	6.5	268	15	US-10-424-599-239014	Sequence 239014, App
783	73.5	6.7	545	16	US-10-437-963-148082	Sequence 148082, A	856	71.5	6.5	300	14	US-10-424-599-175004	Sequence 175004, App
784	73.5	6.7	547	15	US-10-282-122A-60074	Sequence 60074, A	857	71.5	6.5	300	14	US-10-032-214-65	Sequence 65, App
785	73.5	6.7	630	14	US-10-207-655-69	Sequence 69, App	858	71.5	6.5	300	14	US-10-032-214-207	Sequence 207, App
786	73.5	6.7	785	14	US-10-174-677-25	Sequence 25, App	859	71.5	6.5	300	18	US-10-479-901-65	Sequence 65, App
787	73.5	6.7	796	15	US-10-072-012-485	Sequence 485, App	860	71.5	6.5	303	14	US-10-479-901-207	Sequence 207, App
788	73	6.6	14	10	US-09-903-190-28	Sequence 28, App	861	71.5	6.5	303	14	US-10-032-214-51	Sequence 51, App
789	73	6.6	14	14	US-10-319-763-28	Sequence 28, App	862	71.5	6.5	303	14	US-10-032-214-52	Sequence 52, App
790	73	6.6	14	17	US-10-926-683-6	Sequence 6, App	863	71.5	6.5	303	14	US-10-032-214-54	Sequence 54, App
791	73	6.6	14	17	US-10-930-331-28	Sequence 28, App	864	71.5	6.5	303	14	US-10-032-214-55	Sequence 55, App
792	73	6.6	205	10	US-09-919-039-258	Sequence 258, App	865	71.5	6.5	303	14	US-10-032-214-56	Sequence 56, App
793	73	6.6	205	13	US-10-081-218-1	Sequence 1, App	866	71.5	6.5	303	14	US-10-032-214-57	Sequence 57, App
794	73	6.6	205	14	US-10-050-704-98	Sequence 98, App	867	71.5	6.5	303	14	US-10-032-214-58	Sequence 58, App
795	73	6.6	205	16	US-10-424-598-10	Sequence 10, App	868	71.5	6.5	303	14	US-10-032-214-60	Sequence 60, App
796	73	6.6	205	16	US-10-798-512-98	Sequence 98, App	869	71.5	6.5	303	14	US-10-032-214-63	Sequence 63, App
797	73	6.6	221	9	US-09-925-298-603	Sequence 603, App	870	71.5	6.5	303	14	US-10-032-214-66	Sequence 66, App
798	73	6.6	221	14	US-10-102-806-603	Sequence 603, App	871	71.5	6.5	303	14	US-10-032-214-67	Sequence 67, App
799	73	6.6	363	15	US-10-424-599-211602	Sequence 211602, App	872	71.5	6.5	303	14	US-10-032-214-179	Sequence 179, App
800	73	6.6	369	15	US-10-425-114-40320	Sequence 40320, A	873	71.5	6.5	303	14	US-10-032-214-181	Sequence 181, App
801	73	6.6	369	15	US-10-425-114-42082	Sequence 42082, A	874	71.5	6.5	303	14	US-10-032-214-187	Sequence 187, App
802	73	6.6	512	15	US-10-282-122A-63492	Sequence 63492, A	875	71.5	6.5	303	14	US-10-032-214-189	Sequence 189, App
803	73	6.6	540	15	US-10-424-599-231400	Sequence 231400, App	876	71.5	6.5	303	14	US-10-032-214-194	Sequence 194, App
804	73	6.6	679	16	US-10-425-115-323191	Sequence 323191, App	877	71.5	6.5	303	14	US-10-032-214-192	Sequence 192, App
805	73	6.6	1147	15	US-10-872-198-147	Sequence 42, App	878	71.5	6.5	303	14	US-10-032-214-205	Sequence 205, App
806	73	6.6	1148	17	US-10-872-198-147	Sequence 147, App	879	71.5	6.5	303	14	US-10-032-214-208	Sequence 208, App
807	73	6.6	1148	20	US-11-021-951-147	Sequence 147, App	880	71.5	6.5	303	14	US-10-032-214-209	Sequence 209, App
808	73	6.6	1177	17	US-10-461-862-146	Sequence 146, App	881	71.5	6.5	303	14	US-10-032-214-217	Sequence 217, App
809	73	6.6	1179	17	US-10-461-862-148	Sequence 148, App	882	71.5	6.5	303	18	US-10-479-901-51	Sequence 51, App
810	73	6.6	1181	14	US-10-160-354-2	Sequence 2, App	883	71.5	6.5	303	18	US-10-479-901-52	Sequence 52, App
811	73	6.6	1181	15	US-10-295-027-1286	Sequence 1286, App	884	71.5	6.5	303	18	US-10-479-901-54	Sequence 54, App
812	73	6.6	1181	15	US-10-211-462-187	Sequence 187, App	885	71.5	6.5	303	18	US-10-479-901-55	Sequence 55, App
813	73	6.6	1181	16	US-10-783-528-77	Sequence 77, App	886	71.5	6.5	303	18	US-10-479-901-57	Sequence 57, App
814	73	6.6	1181	16	US-10-473-127-280	Sequence 280, App	887	71.5	6.5	303	18	US-10-479-901-58	Sequence 58, App
815	73	6.6	1181	16	US-10-473-127-282	Sequence 282, App	888	71.5	6.5	303	18	US-10-479-901-60	Sequence 60, App
816	73	6.6	1181	16	US-10-473-127-283	Sequence 283, App	889	71.5	6.5	303	18	US-10-479-901-61	Sequence 61, App
817	73	6.6	1181	18	US-10-491-545A-34	Sequence 34, App	890	71.5	6.5	303	18	US-10-479-901-63	Sequence 63, App
818	73	6.6	1181	18	US-10-764-425-139	Sequence 139, App	891	71.5	6.5	303	18	US-10-479-901-66	Sequence 66, App

892	71.5	6.5	303	18	US-10-479-901-67	Sequence 67, Appl	965	71	6.4	493	16	US-10-473-127-1301	Sequence 1301, Ap
893	71.5	6.5	303	18	US-10-479-901-179	Sequence 179, Appl	966	71	6.4	493	16	US-10-473-127-1303	Sequence 1303, Ap
894	71.5	6.5	303	18	US-10-479-901-181	Sequence 181, Appl	967	71	6.4	493	16	US-10-473-127-1305	Sequence 1305, Ap
895	71.5	6.5	303	18	US-10-479-901-187	Sequence 187, Appl	968	71	6.4	493	17	US-10-741-600-1051	Sequence 1051, Ap
896	71.5	6.5	303	18	US-10-479-901-189	Sequence 189, Appl	969	71	6.4	496	14	US-10-238-075-370	Sequence 370, Appl
897	71.5	6.5	303	18	US-10-479-901-194	Sequence 194, Appl	970	71	6.4	496	15	US-10-282-1128A-68885	Sequence 68885, A
898	71.5	6.5	303	18	US-10-479-901-202	Sequence 202, Appl	971	71	6.4	514	15	US-10-309-290-148	Sequence 148, Appl
899	71.5	6.5	303	18	US-10-479-901-205	Sequence 205, Appl	972	71	6.4	535	16	US-10-741-601-336	Sequence 336, Appl
900	71.5	6.5	303	18	US-10-479-901-208	Sequence 208, Appl	973	71	6.4	535	17	US-10-741-600-1044	Sequence 1044, Ap
901	71.5	6.5	303	18	US-10-479-901-209	Sequence 209, Appl	974	71	6.4	560	9	US-09-735-705-225	Sequence 225, Appl
902	71.5	6.5	303	18	US-10-479-901-217	Sequence 217, Appl	975	71	6.4	560	9	US-09-850-716A-225	Sequence 225, Appl
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904	71.5	6.5	450	17	US-10-741-849-7232	Sequence 7232, A	977	71	6.4	560	9	US-09-943-075A-6	Sequence 6, Appl1
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906	71.5	6.5	508	14	US-10-057-136-20	Sequence 20, Appl1	979	71	6.4	560	14	US-10-007-700-225	Sequence 225, Appl
907	71.5	6.5	549	10	US-09-959-845-2	Sequence 2, Appl1	980	71	6.4	560	14	US-10-117-982-225	Sequence 225, Appl
908	71.5	6.5	549	10	US-09-972-268-17	Sequence 17, Appl1	981	71	6.4	560	15	US-10-463-106-2	Sequence 2, Appl1
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910	71.5	6.5	640	16	US-10-437-963-196546	Sequence 196546, Sequence 225, Appl	983	71	6.4	560	15	US-10-313-986-225	Sequence 225, Appl
911	71.5	6.5	796	14	US-10-163-818-4	Sequence 4, Appl1	984	71	6.4	560	15	US-10-309-290-152	Sequence 152, Appl
912	71.5	6.5	796	14	US-10-174-677-11	Sequence 11, Appl1	985	71	6.4	560	16	US-10-408-765A-466	Sequence 466, Appl
913	71.5	6.5	796	15	US-10-457-257-2	Sequence 2, Appl1	986	71	6.4	560	16	US-10-775-972-225	Sequence 225, Appl
914	71.5	6.5	796	15	US-10-072-012-486	Sequence 486, Appl	987	71	6.4	560	16	US-10-723-860-1128	Sequence 1128, Ap
915	71.5	6.5	796	16	US-10-678-160A-4	Sequence 4, Appl1	988	71	6.4	560	18	US-10-922-124-225	Sequence 225, Appl
916	71.5	6.5	796	17	US-10-941-442-4	Sequence 4, Appl1	1036	71	6.4	572	14	US-10-219-065-42	Sequence 42, Appl1
917	71.5	6.5	796	18	US-10-712-892A-22	Sequence 22, Appl1	1093	71	6.4	668	16	US-10-741-601-341	Sequence 341, Appl
918	71.5	6.5	796	18	US-10-712-892A-24	Sequence 24, Appl1	1094	71	6.4	668	16	US-10-473-127-1285	Sequence 1285, Ap
919	71.5	6.5	936	15	US-10-282-122A-58699	Sequence 58699, A	1095	71	6.4	668	17	US-10-741-600-1047	Sequence 1047, Ap
920	71.5	6.5	1139	15	US-10-369-493-5826	Sequence 5826, Ap	1096	71	6.4	668	17	US-10-482-029-253	Sequence 253, Appl
921	71	6.4	183	15	US-10-094-749-2663	Sequence 2663, Ap	1097	71	6.4	676	16	US-10-473-127-1268	Sequence 1268, Ap
922	71	6.4	235	14	US-10-157-031-321	Sequence 321, Appl	1098	71	6.4	676	16	US-10-473-127-1318	Sequence 1318, Ap
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924	71	6.4	235	15	US-10-295-027-1295	Sequence 1295, Ap	1100	71	6.4	686	9	US-09-893-238-13	Sequence 13, Appl1
925	71	6.4	235	15	US-10-295-027-1296	Sequence 1296, Ap	1101	71	6.4	691	16	US-10-741-601-344	Sequence 344, Appl
926	71	6.4	307	20	US-09-781-712B-4	Sequence 4, Appl1	1102	71	6.4	691	16	US-10-473-127-1287	Sequence 1287, Ap
927	71	6.4	307	20	US-11-003-069-4	Sequence 66, Appl1	1103	71	6.4	691	17	US-10-741-600-1053	Sequence 1053, Ap
928	71	6.4	336	15	US-10-403-571-66	Sequence 1271, Ap	1104	71	6.4	699	16	US-10-473-127-1274	Sequence 1274, Ap
929	71	6.4	338	16	US-10-473-127-1315	Sequence 1315, Ap	1105	71	6.4	699	16	US-10-473-127-1280	Sequence 1280, Ap
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931	71	6.4	361	11	US-09-836-544-32	Sequence 32, Appl1	1107	71	6.4	699	17	US-10-696-693-71	Sequence 71, Appl1
932	71	6.4	361	16	US-10-741-601-340	Sequence 340, Appl	1108	71	6.4	700	14	US-10-012-963C-2	Sequence 2, Appl1
933	71	6.4	361	16	US-10-473-127-1273	Sequence 1273, Ap	1109	71	6.4	700	16	US-10-473-127-1306	Sequence 1306, Ap
934	71	6.4	361	16	US-10-473-127-1275	Sequence 1275, Ap	1110	71	6.4	719	16	US-10-473-127-1270	Sequence 1270, Ap
935	71	6.4	361	16	US-10-473-127-1276	Sequence 1276, Ap	1111	71	6.4	719	16	US-10-473-127-1316	Sequence 1316, Ap
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937	71	6.4	361	16	US-10-473-127-1292	Sequence 1292, Ap	1113	71	6.4	742	15	US-10-116-275-206	Sequence 206, Appl
938	71	6.4	361	16	US-10-473-127-1296	Sequence 1296, Ap	1114	71	6.4	742	16	US-10-648-593-176	Sequence 176, Appl
939	71	6.4	361	16	US-10-473-127-1298	Sequence 1298, Ap	1115	71	6.4	742	16	US-10-663-244-1	Sequence 1, Appl1
940	71	6.4	361	16	US-10-473-127-1300	Sequence 1300, Ap	1116	71	6.4	742	16	US-10-741-601-338	Sequence 338, Appl
941	71	6.4	361	16	US-10-473-127-1302	Sequence 1302, Ap	1117	71	6.4	742	16	US-10-741-601-339	Sequence 339, Appl
942	71	6.4	361	16	US-10-473-127-1304	Sequence 1304, Ap	1118	71	6.4	742	16	US-10-473-127-1282	Sequence 1282, Ap
943	71	6.4	361	16	US-10-473-127-1309	Sequence 1309, Ap	1119	71	6.4	742	16	US-10-473-127-1286	Sequence 1286, Ap
944	71	6.4	361	16	US-10-473-127-1310	Sequence 1310, Ap	1120	71	6.4	742	16	US-10-473-127-1311	Sequence 1311, Ap
945	71	6.4	361	17	US-10-741-600-1048	Sequence 1048, Ap	1121	71	6.4	742	16	US-10-473-127-1319	Sequence 1319, Ap
946	71	6.4	361	17	US-10-482-029-255	Sequence 255, Appl	1122	71	6.4	742	17	US-10-690-880-40	Sequence 40, Appl1
947	71	6.4	361	17	US-10-852-335A-131	Sequence 131, Appl	1123	71	6.4	742	17	US-10-741-600-1046	Sequence 1046, Ap
948	71	6.4	395	16	US-10-741-601-345	Sequence 345, Appl	1124	71	6.4	742	17	US-10-741-600-1049	Sequence 1049, Ap
949	71	6.4	395	16	US-10-473-127-1281	Sequence 1281, Appl	1125	71	6.4	742	17	US-10-741-600-1054	Sequence 1054, Ap
950	71	6.4	395	17	US-10-741-600-1052	Sequence 1052, Ap	1126	71	6.4	742	17	US-10-652-981-16	Sequence 16, Appl1
951	71	6.4	425	16	US-10-741-601-337	Sequence 337, Appl	1127	71	6.4	776	16	US-10-425-115-36321	Sequence 36321, Sequence 29, Appl1
952	71	6.4	425	16	US-10-473-127-1283	Sequence 1283, Ap	1128	71	6.4	801	15	US-10-257-174-29	Sequence 29, Appl1
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Searched: 513545 seqs, 74649064 residues

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## SUMMARIES

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1	376	34.1	805	3 US-08-989-299-2	Sequence 2, Appl.
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3	376	34.1	805	4 US-09-407-427-2	Sequence 2, Appl.
4	376	34.1	819	4 US-09-949-016-11284	Sequence 11284, A
5	359	32.6	711	4 US-10-158-847-138	Sequence 138, App
6	289	26.2	681	4 US-10-158-847-140	Sequence 140, App
7	90	8.2	799	1 US-08-188-228-42	Sequence 42, Appl
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9	89.5	8.1	793	1 US-08-188-228-54	Sequence 54, Appl
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141	69	6.3	1119	4	US-09-905-381A-294	Sequence 294, App	214	66.5	6.0	518	4	US-09-795-847B-2	Sequence 2, Appl
142	69	6.3	1119	4	US-09-906-618-294	Sequence 294, App	215	66.5	6.0	518	4	US-09-869-414-2	Sequence 2, Appl
143	68.5	6.2	375	4	US-09-583-110-4530	Sequence 4530, Ap	216	66.5	6.0	518	4	US-09-548-366F-2	Sequence 2, Appl
144	68.5	6.2	392	4	US-09-634-238-260	Sequence 260, App	217	66.5	6.0	518	4	US-09-548-368D-2	Sequence 2, Appl
145	68.5	6.2	522	1	US-08-680-726A-58	Sequence 58, Appl	218	66.5	6.0	518	4	US-09-794-925A-2	Sequence 2, Appl
146	68.5	6.2	522	3	US-09-092-409-58	Sequence 58, Appl	219	66.5	6.0	518	4	US-09-806-194A-2	Sequence 2, Appl
147	68.5	6.2	747	3	US-09-035-648-18	Sequence 18, Appl	220	66.5	6.0	541	4	US-09-949-016-11075	Sequence 11075, A
148	68.5	6.2	747	3	US-09-001-951-18	Sequence 18, Appl	221	66.5	6.0	591	4	US-09-248-796A-14394	Sequence 14394, A
149	68.5	6.2	747	4	US-08-818-829-18	Sequence 18, Appl	222	66.5	6.0	707	3	US-09-228-986-80	Sequence 80, Appl
150	68.5	6.2	1178	1	US-08-199-776-2	Sequence 2, Appl	223	66.5	6.0	1346	3	US-10-101-464A-80	Sequence 80, Appl
151	68.5	6.2	1178	3	US-08-663-731-2	Sequence 2, Appl	224	66.5	6.0	1346	3	US-09-320-878-4	Sequence 4, Appl
152	68.5	6.2	1178	3	US-08-879-338-2	Sequence 2, Appl	225	66.5	6.0	1346	4	US-09-141-908-5	Sequence 5, Appl
153	68.5	6.2	1178	5	PCT-US95-02044-2	Sequence 2, Appl	226	66.5	6.0	1346	4	US-09-657-440-4	Sequence 4, Appl
154	68.5	6.2	1178	4	US-09-293-228B-2	Sequence 2, Appl	227	66	6.0	121	4	US-09-489-039A-13007	Sequence 13007, A
155	68	6.2	265	4	US-09-322-409-49	Sequence 49, Appl	228	66	6.0	353	4	US-09-203-958A-4	Sequence 4, Appl
156	68	6.2	265	4	US-09-451-527-49	Sequence 49, Appl	229	66	6.0	384	2	US-08-833-226-2	Sequence 2, Appl
157	68	6.2	291	4	US-09-322-409-44	Sequence 44, Appl	230	66	6.0	477	4	US-09-248-796A-14922	Sequence 14922, A
158	68	6.2	291	4	US-09-451-527-44	Sequence 44, Appl	231	66	6.0	453	4	US-09-583-110-1555	Sequence 3555, Ap
159	68	6.2	293	4	US-09-540-236-2400	Sequence 2400, Ap	232	66	6.0	482	4	US-09-107-532A-4868	Sequence 4868, Ap
160	68	6.2	2321	4	US-09-230-652-2	Sequence 2, Appl	233	66	6.0	605	3	US-09-394-645-2	Sequence 2, Appl
161	67.5	6.1	209	3	US-09-109-100-16	Sequence 16, Appl	234	66	6.0	605	3	US-09-213-560B-2	Sequence 2, Appl
162	67.5	6.1	278	3	US-08-339-214-16	Sequence 16, Appl	235	66	6.0	718	2	US-08-560-998-12	Sequence 12, Appl
163	67.5	6.1	278	3	US-08-339-214-26	Sequence 26, Appl	236	66	6.0	723	4	US-09-338-352-6928	Sequence 6928, Ap
164	67.5	6.1	278	4	US-09-131-237C-6	Sequence 6, Appl	237	66	6.0	778	4	US-09-338-352-7907	Sequence 7907, Ap
165	67.5	6.1	278	4	US-09-246-129B-6	Sequence 6, Appl	238	66	6.0	956	1	US-08-185-332A-2	Sequence 2, Appl
166	67.5	6.1	365	4	US-09-949-016-6907	Sequence 6907, Ap	239	66	6.0	956	1	US-08-416-523-2	Sequence 2, Appl
167	67.5	6.1	380	4	US-09-540-236-2987	Sequence 2987, Ap	240	66	6.0	966	4	US-08-789-478-2	Sequence 2, Appl
168	67.5	6.1	391	4	US-09-949-016-7325	Sequence 7325, Ap	241	65.5	5.9	268	4	US-09-322-409-33	Sequence 33, Appl
169	67.5	6.1	505	1	US-09-041-075A-8	Sequence 8, Appl	242	65.5	5.9	268	4	US-09-451-527-23	Sequence 23, Appl
170	67.5	6.1	634	4	US-09-418-963-3	Sequence 3, Appl	243	65.5	5.9	269	3	US-09-430-503-2	Sequence 2, Appl
171	67	6.1	69	4	US-09-149-476-606	Sequence 606, App	244	65.5	5.9	269	3	US-09-430-503-6	Sequence 4, Appl
172	67	6.1	95	1	US-08-725-531-1	Sequence 1, Appl	245	65.5	5.9	269	3	US-09-430-503-6	Sequence 4, Appl
173	67	6.1	95	2	US-09-213-392-1	Sequence 1, Appl	246	65.5	5.9	269	3	US-09-430-503-8	Sequence 8, Appl



247	65.5	5.9	294	4	US-09-322-409-7	Sequence 7, Appli	320	64.5	5.9	906	4	US-09-417-039-11	Sequence 11, Appli
248	65.5	5.9	294	4	US-09-451-527-7	Sequence 7, Appli	321	64.5	5.9	913	2	US-08-474-067-6	Sequence 6, Appli
249	65.5	5.9	313	4	US-09-949-016-10974	Sequence 10974, A	322	64.5	5.9	913	2	US-08-474-068A-6	Sequence 6, Appli
250	65.5	5.9	363	4	US-08-914-372C-37	Sequence 37, Appl	323	64.5	5.9	913	2	US-08-472-481-5	Sequence 5, Appli
251	65.5	5.9	364	1	US-08-680-726A-56	Sequence 56, Appl	324	64.5	5.9	1346	3	US-09-105-537-37	Sequence 37, Appl
252	65.5	5.9	364	3	US-09-092-409-56	Sequence 56, Appl	325	64.5	5.9	11877	3	US-09-105-537-6	Sequence 6, Appli
253	65.5	5.9	364	4	US-08-914-372C-11	Sequence 11, Appl	326	64	5.8	150	4	US-09-248-796A-23394	Sequence 23394, A
254	65.5	5.9	367	4	US-09-489-039A-12480	Sequence 12480, A	327	64	5.8	199	4	US-09-902-540-9868	Sequence 9868, Ap
255	65.5	5.9	384	1	US-08-221-730A-11	Sequence 11, Appl	328	64	5.8	231	4	US-09-949-016-7831	Sequence 7831, Ap
256	65.5	5.9	476	4	US-09-538-092-346	Sequence 346, App	329	64	5.8	250	4	US-09-252-991A-33027	Sequence 33027, A
257	65.5	5.9	556	4	US-09-538-092-712	Sequence 712, App	330	64	5.8	329	4	US-09-651-200-19	Sequence 19, Appl
258	65.5	5.9	561	4	US-09-866-510-24	Sequence 24, Appl	331	64	5.8	473	4	US-09-107-532A-5699	Sequence 5699, Ap
259	65.5	5.9	668	4	US-09-949-016-8139	Sequence 8139, Ap	332	64	5.8	332	2	US-08-332-5622A-134	Sequence 134, App
260	65.5	5.9	906	1	US-08-220-151-9	Sequence 9, Appli	333	64	5.8	350	4	US-09-252-991A-30568	Sequence 30568, A
261	65.5	5.9	906	1	US-08-413-118-9	Sequence 9, Appli	334	64	5.8	406	4	US-09-270-767-47219	Sequence 32002, A
262	65.5	5.9	906	3	US-08-473-446-9	Sequence 9, Appli	335	64	5.8	449	4	US-09-640-419C-24	Sequence 47219, A
263	65.5	5.9	1090	4	US-09-866-510-14	Sequence 14, Appl	336	64	5.8	463	4	US-09-107-532A-5699	Sequence 5699, Ap
264	65.5	5.9	1106	1	US-08-180-195-2	Sequence 2, Appli	337	64	5.8	573	4	US-09-535-315-23	Sequence 23, Appl
265	65.5	5.9	1106	1	US-08-168-917-2	Sequence 2, Appli	338	64	5.8	693	4	US-09-336-910A-3	Sequence 3, Appli
266	65.5	5.9	1106	1	US-08-477-329-2	Sequence 2, Appli	339	64	5.8	856	4	US-09-618-353-8	Sequence 8, Appli
267	65.5	5.9	1106	1	US-08-475-458-2	Sequence 2, Appli	340	64	5.8	862	4	US-09-751-687-9	Sequence 9, Appli
268	65.5	5.9	1106	2	US-08-460-510-2	Sequence 2, Appli	341	64	5.8	862	4	US-09-751-687-12	Sequence 12, Appl
269	65.5	5.9	1106	2	US-08-460-490-2	Sequence 2, Appli	342	64	5.8	1026	4	US-09-949-016-7526	Sequence 7526, Ap
270	65.5	5.9	1106	3	US-08-980-400-2	Sequence 2, Appli	343	64	5.8	1212	3	US-09-090-535-2	Sequence 2, Appli
271	65.5	5.9	1106	3	US-08-462-728-4	Sequence 4, Appli	344	64	5.8	1212	3	US-09-090-535-3	Sequence 3, Appli
272	65.5	5.9	1106	3	US-09-583-459A-2	Sequence 2, Appli	345	64	5.8	1212	3	US-09-090-535-4	Sequence 4, Appli
273	65.5	5.9	1106	3	US-09-583-210-2	Sequence 2, Appli	346	64	5.8	1212	3	US-09-090-535-4	Sequence 4, Appli
274	65.5	5.9	1106	3	US-09-583-449A-2	Sequence 2, Appli	347	63.5	5.8	92	4	US-09-640-211A-947	Sequence 947, App
275	65.5	5.9	1106	3	US-09-435-059-2	Sequence 2, Appli	348	63.5	5.8	253	4	US-09-543-681A-8042	Sequence 8042, Ap
276	65.5	5.9	1106	3	US-08-461-917-4	Sequence 4, Appli	349	63.5	5.8	272	4	US-09-949-016-5936	Sequence 5936, Ap
277	65.5	5.9	1106	4	US-08-464-436-4	Sequence 4, Appli	350	63.5	5.8	317	4	US-09-543-681A-4789	Sequence 4789, Ap
278	65.5	5.9	1106	4	US-08-464-436-4	Sequence 4, Appli	351	63.5	5.8	361	4	US-08-914-372C-8	Sequence 8, Appli
279	65.5	5.9	1106	4	US-09-866-510-16	Sequence 16, Appl	352	63.5	5.8	361	4	US-08-914-372C-9	Sequence 9, Appli
280	65.5	5.9	1106	4	US-09-866-510-18	Sequence 18, Appl	353	63.5	5.8	382	4	US-09-248-796A-14294	Sequence 14294, A
281	65.5	5.9	1106	4	US-09-866-510-20	Sequence 20, Appl	354	63.5	5.8	395	4	US-09-550-115-8	Sequence 8, Appli
282	65.5	5.9	1106	4	US-09-866-510-22	Sequence 22, Appl	355	63.5	5.8	431	4	US-09-866-028-83	Sequence 83, Appl
283	65.5	5.9	1106	5	PCT-US92-00730-2	Sequence 2, Appli	356	63.5	5.8	485	3	US-09-944-457-83	Sequence 83, Appl
284	65.5	5.9	1106	5	PCT-US92-00662-2	Sequence 2, Appli	357	63.5	5.8	485	3	US-09-320-878-10	Sequence 10, Appl
285	65.5	5.9	1113	4	US-09-332-522B-2	Sequence 2, Appli	358	63.5	5.8	485	3	US-09-105-537-10	Sequence 10, Appl
286	65	5.9	138	4	US-09-134-000C-6578	Sequence 6578, Ap	359	63.5	5.8	485	3	US-09-141-908-23	Sequence 23, Appl
287	65	5.9	146	4	US-09-582-337-12	Sequence 12, Appl	360	63.5	5.8	485	4	US-09-657-440-10	Sequence 10, Appl
288	65	5.9	156	4	US-09-270-767-33196	Sequence 33196, A	361	63.5	5.8	533	4	US-09-508-370A-6	Sequence 6, Appli
289	65	5.9	156	4	US-09-270-767-48413	Sequence 48413, A	362	63.5	5.8	535	4	US-09-949-016-110290	Sequence 10290, A
290	65	5.9	250	3	US-09-134-001C-4399	Sequence 4399, Ap	363	63.5	5.8	674	4	US-09-949-016-7196	Sequence 7196, Ap
291	65	5.9	330	2	US-08-332-562A-81	Sequence 81, Appl	364	63.5	5.8	681	4	US-09-543-681A-5453	Sequence 5453, Ap
292	65	5.9	448	4	US-09-252-991A-18545	Sequence 18545, A	365	63.5	5.8	699	5	PCT-US94-07297-39	Sequence 39, Appl
293	65	5.9	534	4	US-09-710-279-920	Sequence 920, App	366	63.5	5.8	821	4	US-09-438-165A-155	Sequence 155, App
294	65	5.9	535	4	US-09-326-480A-3	Sequence 3, Appli	367	63.5	5.8	835	4	US-09-619-353-7	Sequence 7, Appli
295	65	5.9	667	1	US-07-879-617A-8	Sequence 8, Appli	368	63.5	5.8	906	4	US-09-367-895-41	Sequence 41, Appl
296	65	5.9	855	1	US-08-753-985-8	Sequence 8, Appli	369	63.5	5.8	921	1	US-08-396-479B-2	Sequence 2, Appli
297	65	5.9	855	1	US-08-336-342A-4	Sequence 4, Appli	370	63.5	5.8	921	1	US-08-818-823-2	Sequence 2, Appli
298	65	5.9	887	4	US-09-949-016-11126	Sequence 11126, A	371	63.5	5.8	980	1	US-08-091-569-2	Sequence 2, Appli
299	65	5.9	1023	4	US-09-514-907A-6	Sequence 6, Appli	372	63.5	5.8	980	1	US-08-203-676-2	Sequence 2, Appli
300	65	5.9	1023	4	US-09-896-994-6	Sequence 6, Appli	373	63.5	5.8	980	2	US-08-822-238-2	Sequence 2, Appli
301	64.5	5.9	137	4	US-09-134-000C-6680	Sequence 6680, Ap	374	63.5	5.8	1171	4	US-09-417-197-131	Sequence 131, App
302	64.5	5.9	171	4	US-09-134-000C-3311	Sequence 4311, Ap	375	63.5	5.8	1181	4	US-09-417-197-133	Sequence 133, App
303	64.5	5.9	228	3	US-08-911-422-6	Sequence 6, Appli	376	63.5	5.8	1330	3	US-09-543-681A-8057	Sequence 8057, Ap
304	64.5	5.9	234	4	US-09-512-363-2	Sequence 2, Appli	377	63.5	5.8	3782	3	US-09-105-537-4	Sequence 56, Appli
305	64.5	5.9	234	4	US-09-176-200-2	Sequence 2, Appli	378	63	5.7	133	4	US-09-861-451A-56	Sequence 172, App
306	64.5	5.9	234	4	US-09-915-593-2	Sequence 2, Appli	379	63	5.7	138	4	US-09-647-468-172	Sequence 8, Appl
307	64.5	5.9	240	4	US-09-512-363-6	Sequence 6, Appli	380	63	5.7	169	4	US-09-524-101D-8	Sequence 8, Appli
308	64.5	5.9	240	4	US-09-176-200-6	Sequence 6, Appli	381	63	5.7	182	4	US-09-328-352-4216	Sequence 4216, Ap
309	64.5	5.9	240	4	US-09-915-593-6	Sequence 6, Appli	382	63	5.7	289	4	US-09-270-767-40192	Sequence 40192, A
310	64.5	5.9	270	3	US-09-085-305-20	Sequence 20, Appl	383	63	5.7	289	4	US-09-270-767-55408	Sequence 55408, A
311	64.5	5.9	357	4	US-09-902-540-9903	Sequence 9903, Ap	384	63	5.7	301	4	US-09-489-039A-9064	Sequence 9064, Ap
312	64.5	5.9	381	4	US-09-540-236-3515	Sequence 3615, Ap	385	63	5.7	302	4	US-09-107-532A-5635	Sequence 5635, Ap
313	64.5	5.9	404	4	US-09-252-991A-18546	Sequence 18546, A	386	63	5.7	310	4	US-09-543-681A-6858	Sequence 6858, Ap
314	64.5	5.9	464	2	US-08-602-725-32	Sequence 32, Appl	387	63	5.7	315	4	US-09-949-016-11121	Sequence 11121, A
315	64.5	5.9	464	4	US-09-949-016-6115	Sequence 6115, Ap	388	63	5.7	315	4	US-09-949-016-11122	Sequence 11122, A
316	64.5	5.9	464	4	US-09-949-016-7525	Sequence 7525, Ap	389	63	5.7	362	6	5504194-2	Patent No. 5504194
317	64.5	5.9	556	4	US-09-248-796A-23187	Sequence 23187, A	390	63	5.7	362	6	5504194-2	Patent No. 5504194
318	64.5	5.9	581	4	US-09-851-985-4	Sequence 4, Appli	391	63	5.7	396	4	US-09-555-062B-2	Sequence 2, Appli
319	64.5	5.9	694	4	US-09-851-985-2	Sequence 2, Appli	392	63	5.7	396	4	US-09-555-062B-4	Sequence 4, Appli

393	63	5.7	452	4	US-09-711-164-366	Sequence 366, App	466	62.5	5.7	888	1	US-08-445-640-35	Sequence 35, App1
394	63	5.7	521	4	US-09-489-039A-8118	Sequence 8118, Ap	467	62.5	5.7	888	3	US-08-170-558-35	Sequence 35, App1
395	63	5.7	632	4	US-09-949-016-10386	Sequence 10386, A	468	62.5	5.7	888	3	US-08-447-314-35	Sequence 35, App1
396	63	5.7	673	4	US-09-583-110-2860	Sequence 2860, Ap	469	62.5	5.7	888	3	US-08-445-461-35	Sequence 35, App1
397	63	5.7	691	4	US-09-107-433-3567	Sequence 3567, Ap	470	62.5	5.7	888	3	US-08-223-490-35	Sequence 35, App1
398	63	5.7	762	3	US-09-228-986-114	Sequence 114, App	471	62.5	5.7	889	1	US-08-372-892-2	Sequence 2, App1
399	63	5.7	762	3	US-10-101-464A-114	Sequence 114, App	472	62.5	5.7	894	1	US-08-445-640-34	Sequence 34, App1
400	63	5.7	934	4	US-10-101-464A-114	Sequence 114, App	473	62.5	5.7	894	1	US-08-170-558-35	Sequence 34, App1
401	63	5.7	762	3	US-09-902-540-14209	Sequence 14209, A	474	62.5	5.7	894	3	US-08-447-314-34	Sequence 34, App1
402	63	5.7	1132	4	US-09-568-784A-87	Sequence 87, App1	475	62.5	5.7	894	3	US-08-445-461-34	Sequence 34, App1
403	63	5.7	1132	4	US-09-568-784A-87	Sequence 87, App1	476	62.5	5.7	894	3	US-08-445-461-34	Sequence 34, App1
404	63	5.7	3031	1	US-07-688-008-2	Sequence 2, App1	477	62.5	5.7	907	1	US-08-223-490-34	Sequence 34, App1
405	62.5	5.7	115	4	US-09-540-236-2698	Sequence 2698, Ap	478	62.5	5.7	907	3	US-08-349-006-2	Sequence 2, App1
406	62.5	5.7	234	4	US-09-492-709A-350	Sequence 350, App	479	62.5	5.7	907	3	US-08-804-439A-19	Sequence 19, App1
407	62.5	5.7	237	4	US-09-248-796A-14858	Sequence 14858, A	480	62.5	5.7	907	3	US-08-720-229-19	Sequence 19, App1
408	62.5	5.7	289	2	US-08-580-545B-4	Sequence 4, App1	481	62.5	5.7	907	3	US-09-171-659-2	Sequence 2, App1
409	62.5	5.7	289	3	US-09-262-653A-4	Sequence 2, App1	482	62.5	5.7	907	5	PCT-US9A-04180-2	Sequence 2, App1
410	62.5	5.7	289	3	US-08-867-484A-2	Sequence 2, App1	483	62.5	5.7	975	4	US-09-949-016-1595	Sequence 7595, Ap
411	62.5	5.7	289	4	US-09-760-882-2	Sequence 2, App1	484	62.5	5.7	1132	4	US-09-248-796A-15026	Sequence 15026, A
412	62.5	5.7	320	3	US-09-256-000-17	Sequence 17, App1	485	62.5	5.7	1333	3	US-09-356-952-2	Sequence 2, App1
413	62.5	5.7	320	4	US-10-034-015A-17	Sequence 17, App1	486	62	5.6	1333	4	US-09-976-594-312	Sequence 312, App
414	62.5	5.7	386	1	US-08-758-213-1	Sequence 1, App1	487	62	5.6	136	4	US-09-647-468-155	Sequence 155, App
415	62.5	5.7	386	2	US-08-692-787-48	Sequence 48, App1	488	62	5.6	145	4	US-09-621-976-4037	Sequence 4037, Ap
416	62.5	5.7	386	3	US-09-097-199-48	Sequence 48, App1	489	62	5.6	220	3	US-08-238-208A-21	Sequence 21, App1
417	62.5	5.7	386	4	US-09-248-796A-15279	Sequence 15279, A	490	62	5.6	223	2	US-08-505-058-5	Sequence 5, App1
418	62.5	5.7	391	4	US-09-949-016-6022	Sequence 6022, Ap	491	62	5.6	223	2	US-08-459-818-25	Sequence 25, App1
419	62.5	5.7	392	4	US-09-583-110-5170	Sequence 5170, Ap	492	62	5.6	223	2	US-08-889-666-25	Sequence 25, App1
420	62.5	5.7	403	4	US-09-107-433-3904	Sequence 3904, Ap	493	62	5.6	223	2	US-08-465-078-25	Sequence 25, App1
421	62.5	5.7	403	4	US-09-489-039A-13550	Sequence 13550, A	494	62	5.6	223	2	US-08-725-776-25	Sequence 25, App1
422	62.5	5.7	413	4	US-09-248-796A-18131	Sequence 18131, A	495	62	5.6	223	2	US-08-488-062-25	Sequence 25, App1
423	62.5	5.7	414	1	US-08-188-228-52	Sequence 52, App1	496	62	5.6	250	4	US-09-322-409-31	Sequence 31, App1
424	62.5	5.7	414	1	US-08-332-643-46	Sequence 46, App1	497	62	5.6	250	4	US-09-451-527-31	Sequence 31, App1
425	62.5	5.7	414	1	US-08-332-638-52	Sequence 52, App1	498	62	5.6	273	4	US-09-910-174B-2	Sequence 2, App1
426	62.5	5.7	421	4	US-09-668-262A-16	Sequence 16, App1	499	62	5.6	273	4	US-09-620-461-2	Sequence 2, App1
427	62.5	5.7	428	4	US-09-173-300-36	Sequence 36, App1	500	62	5.6	276	4	US-09-322-409-26	Sequence 26, App1
428	62.5	5.7	428	4	US-10-027-450-36	Sequence 36, App1	501	62	5.6	276	4	US-09-451-527-26	Sequence 26, App1
429	62.5	5.7	466	3	US-09-256-000-2	Sequence 2, App1	502	62	5.6	294	4	US-09-328-352-6415	Sequence 6415, Ap
430	62.5	5.7	466	3	US-10-034-015A-2	Sequence 2, App1	503	62	5.6	307	2	US-08-332-562A-83	Sequence 83, App1
431	62.5	5.7	476	4	US-09-248-796A-20470	Sequence 20470, A	504	62	5.6	331	4	US-09-107-433-1138	Sequence 3138, Ap
432	62.5	5.7	481	4	US-09-603-208A-2	Sequence 2, App1	505	62	5.6	352	4	US-09-203-958A-2	Sequence 2, App1
433	62.5	5.7	487	4	US-09-562-930-2	Sequence 2, App1	506	62	5.6	357	1	US-08-145-006C-12	Sequence 12, App1
434	62.5	5.7	505	3	US-09-387-256-16	Sequence 16, App1	507	62	5.6	357	5	PCT-US9A-00545-12	Sequence 12, App1
435	62.5	5.7	505	3	US-09-395-115-16	Sequence 16, App1	508	62	5.6	365	4	US-09-270-767-44811	Sequence 36811, A
436	62.5	5.7	505	3	US-08-123-934A-8	Sequence 8, App1	509	62	5.6	365	4	US-09-270-767-50028	Sequence 50028, A
437	62.5	5.7	505	3	US-08-436-265-16	Sequence 16, App1	510	62	5.6	376	1	US-08-614-801A-6	Sequence 6, App1
438	62.5	5.7	505	3	US-09-679-187-16	Sequence 16, App1	511	62	5.6	393	4	US-09-949-016-6572	Sequence 6572, Ap
439	62.5	5.7	505	4	US-09-874-628-8	Sequence 8, App1	512	62	5.6	412	3	US-09-134-001C-4885	Sequence 4885, Ap
440	62.5	5.7	505	4	US-09-267-963D-16	Sequence 16, App1	513	62	5.6	431	4	US-09-949-016-10578	Sequence 10578, A
441	62.5	5.7	505	5	PCT-US9A-10080-8	Sequence 8, App1	514	62	5.6	462	4	US-09-949-016-8272	Sequence 8272, Ap
442	62.5	5.7	513	4	US-09-489-039A-9245	Sequence 9245, Ap	515	62	5.6	483	4	US-09-336-115C-20	Sequence 20, App1
443	62.5	5.7	515	2	US-09-146-283-2	Sequence 2, App1	516	62	5.6	630	4	US-10-335-975A-38	Sequence 38, App1
444	62.5	5.7	515	3	US-08-579-823A-2	Sequence 2, App1	517	62	5.6	642	4	US-09-248-796A-14875	Sequence 14875, A
445	62.5	5.7	515	3	US-09-344-195-2	Sequence 2, App1	518	62	5.6	685	4	US-10-101-464A-918	Sequence 918, App
446	62.5	5.7	533	3	US-09-256-000-19	Sequence 19, App1	519	62	5.6	834	1	US-08-471-033-21	Sequence 21, App1
447	62.5	5.7	533	4	US-10-034-015A-19	Sequence 19, App1	520	62	5.6	834	2	US-08-471-044-21	Sequence 21, App1
448	62.5	5.7	554	4	US-09-543-681A-5774	Sequence 5774, Ap	521	62	5.6	834	2	US-08-453-483A-21	Sequence 21, App1
449	62.5	5.7	580	3	US-09-256-000-21	Sequence 21, App1	522	62	5.6	834	2	US-08-471-046A-21	Sequence 21, App1
450	62.5	5.7	580	3	US-10-034-015A-21	Sequence 21, App1	523	62	5.6	834	2	US-08-470-566B-21	Sequence 21, App1
451	62.5	5.7	593	2	US-08-987-466-1	Sequence 1, App1	524	62	5.6	834	2	US-08-469-334-21	Sequence 21, App1
452	62.5	5.7	593	3	US-09-240-359-11	Sequence 11, App1	525	62	5.6	834	3	US-09-300-529-21	Sequence 21, App1
453	62.5	5.7	613	4	US-09-949-016-11085	Sequence 11085, A	526	62	5.6	885	4	US-08-372-892-41	Sequence 41, App1
454	62.5	5.7	635	4	US-09-538-092-1	Sequence 1, App1	527	62	5.6	885	4	US-09-919-497-52	Sequence 52, App1
455	62.5	5.7	635	4	US-10-101-464A-932	Sequence 932, App	528	62	5.6	973	4	US-09-252-991A-28749	Sequence 28749, A
456	62.5	5.7	645	4	US-09-345-473E-15	Sequence 15, App1	529	62	5.6	1073	1	US-07-655-564-1	Sequence 1, App1
457	62.5	5.7	645	4	US-09-345-473E-16	Sequence 16, App1	530	62	5.6	1073	1	US-08-241-187-1	Sequence 1, App1
458	62.5	5.7	649	3	US-09-188-930-305	Sequence 305, App	531	62	5.6	1969	4	US-09-418-710-72	Sequence 71, App1
459	62.5	5.7	649	4	US-09-312-283C-305	Sequence 305, App	532	61.5	5.6	143	4	US-09-839-479-71	Sequence 71, App1
460	62.5	5.7	653	1	US-08-188-228-46	Sequence 46, App1	533	61.5	5.6	143	4	US-09-270-767-35507	Sequence 35507, A
461	62.5	5.7	653	1	US-08-332-638-46	Sequence 46, App1	534	61.5	5.6	176	4	US-09-270-767-50724	Sequence 50724, A
462	62.5	5.7	662	4	US-09-949-016-10298	Sequence 10298, A	535	61.5	5.6	216	4	US-09-540-236-3039	Sequence 3039, App
463	62.5	5.7	672	4	US-10-162-012-30	Sequence 30, App1	536	61.5	5.6	216	5	US-09-354-221-6	Sequence 6, App1
464	62.5	5.7	721	4	US-09-248-796A-16667	Sequence 16667, A	537	61.5	5.6	241	5	PCT-US96-121299-2	Sequence 2, App1
465	62.5	5.7	816	4	US-09-949-016-7437	Sequence 7437, Ap	538	61.5	5.6	241	4	US-08-911-423-4	Sequence 4, App1

539	61.5	5.6	241	4	US-09-512-363-28	Sequence 28, Appl	612	61	5.5	764	4	US-09-270-767-45772	Sequence 45772, A
540	61.5	5.6	241	4	US-09-176-200-4	Sequence 4, Appl1	613	61	5.5	780	4	US-09-785-381-11	Sequence 11, Appl1
541	61.5	5.6	241	4	US-09-915-593-4	Sequence 4, Appl1	614	61	5.5	820	4	US-09-489-039A-10142	Sequence 10142, A
542	61.5	5.6	241	4	US-09-915-593-28	Sequence 28, Appl1	615	61	5.5	892	4	US-09-248-796A-15642	Sequence 15642, A
543	61.5	5.6	241	4	US-09-248-796A-17312	Sequence 17312, A	616	61	5.5	925	1	US-08-252-995D-4	Sequence 4, Appl1
544	61.5	5.6	241	4	US-09-949-016-7232	Sequence 7232, Ap	617	61	5.5	1210	2	US-08-834-108-4	Sequence 4, Appl1
545	61.5	5.6	302	4	US-09-328-352-4508	Sequence 4508, Ap	618	61	5.5	1210	4	US-09-949-016-6801	Sequence 6801, Ap
546	61.5	5.6	325	4	US-09-215-569B-6	Sequence 6, Appl1	619	60.5	5.5	178	4	US-09-543-681A-7183	Sequence 7183, Ap
547	61.5	5.6	366	4	US-09-328-352-6796	Sequence 6796, Ap	620	60.5	5.5	199	4	US-09-270-767-31722	Sequence 31722, A
548	61.5	5.6	399	4	US-09-470-767-44122	Sequence 44122, A	621	60.5	5.5	199	4	US-09-270-767-46939	Sequence 46939, A
549	61.5	5.6	404	4	US-09-538-092-50	Sequence 50, Appl	622	60.5	5.5	209	3	US-09-109-100-15	Sequence 15, Appl1
550	61.5	5.6	455	4	US-09-270-767-46029	Sequence 46029, A	623	60.5	5.5	233	2	US-09-024-848-4	Sequence 4, Appl1
551	61.5	5.6	498	4	US-09-107-532A-7077	Sequence 7077, Ap	624	60.5	5.5	233	2	US-09-348-116A-4	Sequence 4, Appl1
552	61.5	5.6	501	1	US-08-149-105-15	Sequence 15, Appl	625	60.5	5.5	236	2	US-08-070-116A-2	Sequence 2, Appl1
553	61.5	5.6	501	1	US-08-317-847-15	Sequence 8, Appl1	626	60.5	5.5	236	1	US-08-557-050-2	Sequence 2, Appl1
554	61.5	5.6	505	3	US-09-382-256-8	Sequence 8, Appl1	627	60.5	5.5	241	1	US-08-188-228-56	Sequence 56, Appl1
555	61.5	5.6	505	3	US-09-395-115-8	Sequence 8, Appl1	628	60.5	5.5	241	1	US-08-332-643-50	Sequence 50, Appl1
556	61.5	5.6	505	3	US-08-436-265-8	Sequence 8, Appl1	629	60.5	5.5	241	1	US-08-332-638-56	Sequence 56, Appl1
557	61.5	5.6	505	3	US-09-679-187-8	Sequence 8, Appl1	630	60.5	5.5	245	4	US-09-248-796A-14382	Sequence 14382, A
558	61.5	5.6	505	4	US-09-267-963D-8	Sequence 8, Appl1	631	60.5	5.5	285	4	US-09-270-767-43451	Sequence 43451, A
559	61.5	5.6	505	4	US-09-949-016-10260	Sequence 10260, A	632	60.5	5.5	292	2	US-09-024-848-2	Sequence 2, Appl1
560	61.5	5.6	505	4	US-09-949-016-10261	Sequence 10261, A	633	60.5	5.5	292	3	US-09-348-116A-2	Sequence 2, Appl1
561	61.5	5.6	505	4	US-09-949-016-10262	Sequence 10262, A	634	60.5	5.5	292	3	US-09-345-468-18	Sequence 18, Appl1
562	61.5	5.6	631	4	US-09-579-664B-11	Sequence 11, Appl	635	60.5	5.5	301	4	US-09-414-453A-18	Sequence 18, Appl1
563	61.5	5.6	631	4	US-10-355-975A-11	Sequence 11, Appl	636	60.5	5.5	301	4	US-09-270-767-33112	Sequence 33112, A
564	61.5	5.6	793	4	US-09-107-532A-5141	Sequence 5141, Ap	637	60.5	5.5	301	4	US-09-270-767-48329	Sequence 48329, A
565	61.5	5.6	825	4	US-09-321-667-16	Sequence 16, Appl	638	60.5	5.5	313	3	US-09-345-468-16	Sequence 16, Appl1
566	61.5	5.6	825	4	US-09-949-001-14	Sequence 14, Appl	639	60.5	5.5	313	3	US-09-414-453A-16	Sequence 16, Appl1
567	61.5	5.6	826	4	US-09-687-050-6	Sequence 6, Appl1	640	60.5	5.5	347	4	US-09-107-433-2714	Sequence 2714, Ap
568	61.5	5.6	839	4	US-09-949-001-26	Sequence 26, Appl	641	60.5	5.5	364	4	US-08-914-372C-10	Sequence 10, Appl1
569	61.5	5.6	4968	4	US-09-424-783-5	Sequence 5, Appl1	642	60.5	5.5	370	4	US-09-583-110-4976	Sequence 4976, Ap
570	61	5.5	273	1	US-08-252-995D-10	Sequence 10, Appl	643	60.5	5.5	376	1	US-08-253-155A-13	Sequence 33, Appl1
571	61	5.5	273	2	US-08-834-108-10	Sequence 10, Appl	644	60.5	5.5	380	4	US-09-270-767-44518	Sequence 44518, A
572	61	5.5	303	4	US-09-252-991A-31930	Sequence 31930, A	645	60.5	5.5	398	4	US-09-192-012-2	Sequence 2, Appl1
573	61	5.5	369	4	US-08-462-509B-4	Sequence 4, Appl1	646	60.5	5.5	447	3	US-09-370-253-10	Sequence 10, Appl1
574	61	5.5	369	5	US-08-462-509B-4	Sequence 4, Appl1	647	60.5	5.5	449	4	US-09-583-110-3602	Sequence 3602, Ap
575	61	5.5	372	5	US-08-462-509B-6	Sequence 6, Appl1	648	60.5	5.5	457	4	US-09-595-990A-2	Sequence 2, Appl1
576	61	5.5	377	5	US-08-846-705-2	Sequence 6, Appl1	649	60.5	5.5	470	4	US-09-107-433-2658	Sequence 2658, Ap
577	61	5.5	389	2	US-08-846-705-2	Sequence 2, Appl1	650	60.5	5.5	482	4	US-09-538-092-1345	Sequence 1345, Ap
578	61	5.5	389	2	US-09-211-823C-23	Sequence 23, Appl	651	60.5	5.5	513	4	US-09-270-767-31725	Sequence 31725, A
579	61	5.5	402	3	US-08-846-704-4	Sequence 4, Appl1	652	60.5	5.5	513	4	US-09-270-767-52492	Sequence 52492, A
580	61	5.5	402	3	US-08-462-509B-2	Sequence 2, Appl1	653	60.5	5.5	544	4	US-09-489-039A-14296	Sequence 14296, A
581	61	5.5	402	5	US-08-462-509B-2	Sequence 2, Appl1	654	60.5	5.5	633	4	US-09-489-039A-13729	Sequence 13729, A
582	61	5.5	416	1	US-08-252-995D-2	Sequence 12692, A	655	60.5	5.5	864	4	US-09-810-268-3	Sequence 3, Appl1
583	61	5.5	416	1	US-08-834-108-2	Sequence 2, Appl1	656	60.5	5.5	948	4	US-09-248-796A-19297	Sequence 19297, A
584	61	5.5	416	1	US-08-834-108-2	Sequence 2, Appl1	657	60.5	5.5	958	4	US-09-706-594-5	Sequence 5, Appl1
585	61	5.5	419	1	US-08-385-186-4	Sequence 4, Appl1	658	60.5	5.5	1051	4	US-09-949-016-6190	Sequence 6190, Ap
586	61	5.5	425	3	US-09-328-352-6670	Sequence 6670, Ap	659	60	5.4	234	4	US-09-252-991A-17003	Sequence 17003, A
587	61	5.5	425	3	US-08-846-704-2	Sequence 2, Appl1	660	60	5.4	238	4	US-09-489-039A-12131	Sequence 12131, A
588	61	5.5	425	3	US-09-479-128-2	Sequence 2, Appl1	661	60	5.4	274	3	US-09-949-016-11628	Sequence 11628, A
589	61	5.5	425	4	US-09-211-823C-22	Sequence 22, Appl	662	60	5.4	274	3	US-09-570-367C-19	Sequence 19, Appl1
590	61	5.5	425	4	US-09-826-509-549	Sequence 549, App	663	60	5.4	274	3	US-09-915-524-19	Sequence 19, Appl1
591	61	5.5	430	4	US-09-198-452A-1038	Sequence 1038, Ap	664	60	5.4	281	4	US-09-934-634-19	Sequence 19, Appl1
592	61	5.5	436	4	US-09-438-185A-968	Sequence 968, App	665	60	5.4	284	4	US-10-101-464A-518	Sequence 518, Appl
593	61	5.5	464	1	US-08-252-995D-6	Sequence 6, Appl1	666	60	5.4	306	4	US-09-270-767-38494	Sequence 38494, A
594	61	5.5	464	2	US-08-834-108-6	Sequence 6, Appl1	667	60	5.4	306	4	US-09-270-767-53711	Sequence 53711, A
595	61	5.5	500	4	US-09-489-039A-10995	Sequence 10995, A	668	60	5.4	325	4	US-09-198-452A-992	Sequence 992, Appl
596	61	5.5	510	1	US-08-249-112-3	Sequence 3, Appl1	669	60	5.4	331	4	US-09-438-185A-922	Sequence 922, App
597	61	5.5	510	5	US-09-907-794A-250	Sequence 250, App	670	60	5.4	336	4	US-09-248-796A-24750	Sequence 24750, A
598	61	5.5	546	4	US-09-905-125A-250	Sequence 250, App	671	60	5.4	335	2	US-08-846-762-93	Sequence 93, Appl
599	61	5.5	546	4	US-09-905-125A-250	Sequence 250, App	672	60	5.4	370	4	US-09-134-000C-5739	Sequence 5739, Appl
600	61	5.5	546	4	US-09-902-775A-250	Sequence 250, App	673	60	5.4	376	4	US-09-902-540-13960	Sequence 13960, A
601	61	5.5	546	4	US-09-906-700-250	Sequence 250, App	674	60	5.4	377	4	US-09-328-352-7154	Sequence 7154, Ap
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603	61	5.5	546	4	US-09-904-920A-250	Sequence 250, App	676	60	5.4	414	4	US-09-710-279-806	Sequence 806, App
604	61	5.5	546	4	US-09-909-064-250	Sequence 250, App	677	60	5.4	415	4	US-09-543-681A-7191	Sequence 7191, Appl
605	61	5.5	546	4	US-09-905-381A-250	Sequence 250, App	678	60	5.4	423	3	US-09-134-001C-3599	Sequence 3599, Ap
606	61	5.5	554	4	US-09-906-618-250	Sequence 250, App	679	60	5.4	428	3	US-09-054-680-5	Sequence 5, Appl1
607	61	5.5	554	4	US-09-614-891-11	Sequence 11, Appl	680	60	5.4	428	4	US-10-029-715-5	Sequence 5, Appl1
608	61	5.5	597	3	US-08-844-274-12	Sequence 12, Appl	681	60	5.4	435	4	US-09-252-991A-1813	Sequence 1813, A
609	61	5.5	597	4	US-09-598-421-12	Sequence 12, Appl	682	60	5.4	443	4	US-09-489-039A-10189	Sequence 10189, A
610	61	5.5	639	4	US-09-270-767-61294	Sequence 61294, A	683	60	5.4	502	4	US-09-902-540-11457	Sequence 11457, A
611	61	5.5	662	4	US-09-134-000C-5682	Sequence 5682, Ap	684	60	5.4	505	1	US-08-149-105-16	Sequence 16, Appl1

665	60	5.4	505	1	US-08-317-847-16	Sequence 16, Appl	758	59.5	5.4	378	4	US-09-489-039A-10110	Sequence 10110, A
666	60	5.4	523	4	US-09-540-236-2599	Sequence 2599, Ap	759	59.5	5.4	380	1	US-08-227-108-16	Sequence 16, Appl
667	60	5.4	540	4	US-09-270-767-35182	Sequence 35182, A	760	59.5	5.4	380	1	US-09-073-674-16	Sequence 16, Appl
668	60	5.4	540	4	US-09-270-767-50399	Sequence 50399, A	761	59.5	5.4	398	4	US-09-348-930A-9	Sequence 9, Appl
669	60	5.4	544	4	US-09-540-236-2905	Sequence 2905, Ap	762	59.5	5.4	398	4	US-09-578-063-75	Sequence 75, Appl
690	60	5.4	592	3	US-08-867-611-47	Sequence 47, Appl	763	59.5	5.4	414	1	US-08-614-801A-4	Sequence 4, Appl
691	60	5.4	592	3	US-09-690-359-47	Sequence 47, Appl	764	59.5	5.4	425	1	US-09-540-236-2213	Sequence 2213, Ap
692	60	5.4	597	3	US-08-867-611-16	Sequence 16, Appl	765	59.5	5.4	415	1	US-08-385-186-13	Sequence 13, Appl
693	60	5.4	597	3	US-09-690-359-16	Sequence 16, Appl	766	59.5	5.4	433	4	US-09-489-039A-9762	Sequence 9762, Ap
694	60	5.4	597	5	PCT-US92-06965A-21	Sequence 21, Appl	767	59.5	5.4	492	4	US-09-902-540-13917	Sequence 13917, A
695	60	5.4	677	4	US-10-101-464A-891	Sequence 891, App	768	59.5	5.4	502	3	US-09-382-256-12	Sequence 12, Appl
696	60	5.4	690	3	US-08-816-977-47	Sequence 47, Appl	769	59.5	5.4	502	3	US-09-335-115-12	Sequence 12, Appl
697	60	5.4	690	3	US-09-334-477-47	Sequence 47, Appl	770	59.5	5.4	502	3	US-08-436-265-12	Sequence 12, Appl
698	60	5.4	694	3	US-08-816-977-49	Sequence 49, Appl	771	59.5	5.4	502	3	US-09-679-187-12	Sequence 12, Appl
699	60	5.4	694	4	US-09-334-477-49	Sequence 49, Appl	772	59.5	5.4	502	4	US-09-267-963D-12	Sequence 12, Appl
700	60	5.4	703	4	US-09-252-991A-26000	Sequence 26000, A	773	59.5	5.4	675	3	US-09-171-878-1	Sequence 1, Appl
701	60	5.4	903	4	US-09-543-681A-4186	Sequence 4186, Ap	774	59.5	5.4	717	4	US-10-101-464A-810	Sequence 810, App
702	60	5.4	981	4	US-09-902-540-16812	Sequence 16812, A	775	59.5	5.4	728	4	US-09-949-016-10391	Sequence 10391, A
703	60	5.4	1091	1	US-07-695-564-3	Sequence 3, Appl	776	59.5	5.4	739	4	US-09-854-845-45	Sequence 45, Appl
704	60	5.4	1091	1	US-08-241-387-3	Sequence 3, Appl	777	59.5	5.4	744	4	US-09-854-845-43	Sequence 43, Appl
705	60	5.4	1241	3	US-09-040-774-2	Sequence 2, Appl	778	59.5	5.4	776	4	US-09-165-396-3	Sequence 3, Appl
706	60	5.4	1253	3	US-08-864-785-2	Sequence 2, Appl	779	59.5	5.4	802	4	US-09-889-746-4	Sequence 4, Appl
707	60	5.4	1375	3	US-09-210-361-4	Sequence 4, Appl	780	59.5	5.4	838	4	US-09-854-845-29	Sequence 29, Appl
708	60	5.4	1375	4	US-09-740-274-4	Sequence 4, Appl	781	59.5	5.4	843	4	US-09-854-845-27	Sequence 27, Appl
709	60	5.4	2319	1	US-08-212-133A-8	Sequence 8, Appl	782	59.5	5.4	864	4	US-09-751-687-18	Sequence 18, Appl
710	60	5.4	2319	2	US-08-474-503-6	Sequence 6, Appl	783	59.5	5.4	897	1	US-07-960-389-2	Sequence 2, Appl
711	60	5.4	2319	1	US-08-670-707A-6	Sequence 6, Appl	784	59.5	5.4	1038	4	US-09-215-569B-12	Sequence 12, Appl
712	60	5.4	2319	3	US-09-037-601-6	Sequence 6, Appl	785	59.5	5.4	1187	1	US-08-201-697-2	Sequence 2, Appl
713	60	5.4	2319	3	US-09-315-179-6	Sequence 6, Appl	786	59.5	5.4	1282	4	US-09-543-681A-5419	Sequence 5419, Ap
714	60	5.4	2319	3	US-09-523-656-28	Sequence 28, Appl	787	59.5	5.4	1284	2	US-08-286-819A-28	Sequence 28, Appl
715	60	5.4	2319	5	PCT-US94-13200-6	Sequence 6, Appl	788	59.5	5.4	2254	2	US-08-960-357-8	Sequence 8, Appl
716	59.5	5.4	209	3	US-09-109-100-9	Sequence 9, Appl	789	59.5	5.4	2254	3	US-08-960-357-8	Sequence 8, Appl
717	59.5	5.4	209	3	US-09-109-100-11	Sequence 11, Appl	790	59.5	5.4	84	4	US-09-134-001C-3555	Sequence 3555, Ap
718	59.5	5.4	209	3	US-09-109-100-11	Sequence 11, Appl	791	59.5	5.4	88	4	US-09-489-039A-8639	Sequence 8639, Ap
719	59.5	5.4	209	3	US-09-109-100-12	Sequence 12, Appl	792	59.5	5.4	117	3	US-08-973-068-5	Sequence 5, Appl
720	59.5	5.4	209	3	US-09-109-100-13	Sequence 13, Appl	793	59.5	5.4	146	2	US-08-449-287-10	Sequence 10, Appl
721	59.5	5.4	209	3	US-09-109-100-17	Sequence 17, Appl	794	59.5	5.4	187	4	US-09-248-796A-16076	Sequence 16076, A
722	59.5	5.4	209	3	US-09-109-100-18	Sequence 18, Appl	795	59.5	5.4	189	3	US-09-332-934-13	Sequence 13, Appl
723	59.5	5.4	212	3	US-09-109-100-10	Sequence 10, Appl	796	59.5	5.4	189	4	US-09-949-016-6103	Sequence 6103, Ap
724	59.5	5.4	219	2	US-08-902-516-2	Sequence 2, Appl	797	59.5	5.4	205	4	US-09-270-767-05123	Sequence 40123, A
725	59.5	5.4	219	4	US-09-847-185-2	Sequence 2, Appl	798	59.5	5.4	205	4	US-09-270-767-55339	Sequence 55339, A
726	59.5	5.4	229	4	US-09-270-767-11871	Sequence 41871, A	799	59.5	5.4	237	4	US-09-583-110-3141	Sequence 3141, Ap
727	59.5	5.4	229	4	US-09-270-767-57115	Sequence 57115, A	800	59.5	5.4	242	4	US-09-902-540-13487	Sequence 13487, A
728	59.5	5.4	231	1	US-08-220-379B-7	Sequence 7, Appl	801	59.5	5.4	245	3	US-09-413-814-6	Sequence 6, Appl
729	59.5	5.4	231	1	US-08-243-545-2	Sequence 2, Appl	802	59.5	5.4	257	4	US-09-107-433-2806	Sequence 2806, Ap
730	59.5	5.4	231	1	US-08-993-962-2	Sequence 2, Appl	803	59.5	5.4	257	4	US-09-148-796A-20148	Sequence 20148, A
731	59.5	5.4	231	3	US-09-160-841-2	Sequence 2, Appl	804	59.5	5.4	281	3	US-09-134-001C-4763	Sequence 4763, Ap
732	59.5	5.4	231	4	US-08-663-692-2	Sequence 2, Appl	805	59.5	5.4	295	4	US-09-489-039A-8783	Sequence 8783, Ap
733	59.5	5.4	231	4	US-08-444-626-2	Sequence 2, Appl	806	59.5	5.4	301	4	US-09-489-039A-10251	Sequence 10251, A
734	59.5	5.4	231	5	PCT-US94-05365-2	Sequence 2, Appl	807	59.5	5.4	306	4	US-09-270-767-43575	Sequence 43575, A
735	59.5	5.4	231	5	PCT-US95-03866-6	Sequence 6, Appl	808	59.5	5.4	311	4	US-09-270-767-32957	Sequence 32957, A
736	59.5	5.4	235	1	US-08-243-545-6	Sequence 6, Appl	809	59.5	5.4	323	4	US-09-270-767-48174	Sequence 48174, A
737	59.5	5.4	235	2	US-08-993-962-6	Sequence 6, Appl	810	59.5	5.4	323	4	US-09-292-858B-22	Sequence 22, Appl
738	59.5	5.4	235	3	US-09-160-841-6	Sequence 6, Appl	811	59.5	5.4	343	4	US-09-734-237B-35	Sequence 35, Appl
739	59.5	5.4	235	3	US-09-109-100-1	Sequence 1, Appl	812	59.5	5.4	343	4	US-09-734-237B-37	Sequence 37, Appl
740	59.5	5.4	235	3	US-08-669-692-6	Sequence 6, Appl	813	59.5	5.4	355	4	US-09-543-681A-5929	Sequence 5929, Ap
741	59.5	5.4	235	4	US-08-444-626-6	Sequence 6, Appl	814	59.5	5.4	363	4	US-09-107-532A-6757	Sequence 6757, Ap
742	59.5	5.4	235	5	PCT-US94-05365-6	Sequence 6, Appl	815	59.5	5.4	366	1	US-08-004-492-8	Sequence 8, Appl
743	59.5	5.4	238	4	US-09-270-767-31899	Sequence 31899, A	816	59.5	5.4	371	4	US-09-328-352-6825	Sequence 6825, Ap
744	59.5	5.4	238	4	US-09-270-767-47116	Sequence 47116, A	817	59.5	5.4	388	4	US-09-492-709A-378	Sequence 378, App
745	59.5	5.4	247	4	US-09-949-016-11350	Sequence 11350, A	818	59.5	5.4	407	4	US-09-543-681A-7929	Sequence 7929, Ap
746	59.5	5.4	263	3	US-09-134-001C-4998	Sequence 4998, Ap	819	59.5	5.4	416	2	US-08-867-030B-12	Sequence 12, Appl
747	59.5	5.4	264	4	US-09-107-532A-6300	Sequence 6300, Ap	820	59.5	5.4	416	5	PCT-US95-06119-12	Sequence 12, Appl
748	59.5	5.4	269	4	US-10-000-489-78	Sequence 78, Appl	821	59.5	5.4	428	4	US-09-385-219A-6	Sequence 6, Appl
749	59.5	5.4	271	4	US-09-479-040-23	Sequence 23, Appl	822	59.5	5.4	447	1	US-09-937-609-29	Sequence 29, Appl
750	59.5	5.4	274	4	US-09-134-000C-6450	Sequence 6450, Ap	823	59.5	5.4	447	3	US-07-978-892A-6	Sequence 6, Appl
751	59.5	5.4	292	4	US-09-215-569B-2	Sequence 2, Appl	824	59.5	5.4	447	3	US-08-029-170-29	Sequence 29, Appl
752	59.5	5.4	304	4	US-09-328-352-6202	Sequence 6202, Ap	825	59.5	5.4	447	4	US-09-443-745-29	Sequence 29, Appl
753	59.5	5.4	315	4	US-09-949-016-7014	Sequence 7014, Ap	826	59.5	5.4	448	1	US-08-570-157-3	Sequence 3, Appl
754	59.5	5.4	325	4	US-09-215-569B-4	Sequence 4, Appl	827	59.5	5.4	448	3	US-09-076-510-3	Sequence 3, Appl
755	59.5	5.4	354	1	US-09-393-627B-28	Sequence 28, Appl	828	59.5	5.4	449	4	US-09-004-349-3	Sequence 3, Appl
756	59.5	5.4	364	1	US-08-385-186-9	Sequence 9, Appl	829	59.5	5.4	449	4	US-09-198-452A-575	Sequence 575, App
757	59.5	5.4	368	5	PCT-US93-11703-24	Sequence 24, Appl	830	59.5	5.4	453	1	US-07-937-609-26	Sequence 26, Appl

831	59	5.4	453	3	US-08-029-170-26	Sequence 26, Appl	904	58.5	5.3	760	4	US-09-328-352-7293	Sequence 7293, Ap
832	59	5.4	453	4	US-09-443-745-26	Sequence 26, Appl	905	58.5	5.3	807	4	US-09-538-097-574	Sequence 574, App
833	59	5.4	464	4	US-09-438-188A-538	Sequence 538, App	906	58.5	5.3	854	4	US-09-206-551-16	Sequence 16, Appl
834	59	5.4	510	4	US-09-711-164-365	Sequence 365, Appl	907	58.5	5.3	864	2	US-08-620-699A-2	Sequence 2, Appl1
835	59	5.4	519	3	US-09-522-217-85	Sequence 85, Appl	908	58.5	5.3	864	3	US-09-022-255-2	Sequence 2, Appl1
836	59	5.4	519	4	US-09-923-246-85	Sequence 85, Appl	909	58.5	5.3	864	3	US-09-022-696-2	Sequence 2, Appl1
837	59	5.4	519	4	US-10-295-723-85	Sequence 85, Appl	910	58.5	5.3	864	3	US-08-978-773-2	Sequence 2, Appl1
838	59	5.4	575	4	US-09-134-000C-5478	Sequence 5478, Ap	911	58.5	5.3	864	3	US-09-022-255-2	Sequence 2, Appl1
839	59	5.4	596	3	US-09-134-001C-3363	Sequence 3363, Ap	912	58.5	5.3	864	3	US-09-022-260-2	Sequence 2, Appl1
840	59	5.4	600	4	US-09-388-743-22	Sequence 22, Appl	913	58.5	5.3	864	3	US-09-022-257-2	Sequence 2, Appl1
841	59	5.4	600	4	US-10-044-543-22	Sequence 22, Appl	914	58.5	5.3	864	3	US-09-022-257-2	Sequence 2, Appl1
842	59	5.4	653	4	US-09-520-781-10	Sequence 10, Appl	915	58.5	5.3	864	3	US-09-549-679-2	Sequence 2, Appl1
843	59	5.4	667	4	US-09-248-796A-19663	Sequence 19663, A	916	58.5	5.3	921	4	US-09-248-796A-18057	Sequence 18057, A
844	59	5.4	747	4	US-09-949-016-6821	Sequence 6821, Ap	917	58.5	5.3	956	4	US-09-107-532A-5007	Sequence 5007, Ap
845	59	5.4	764	4	US-09-949-016-9890	Sequence 9890, Ap	918	58.5	5.3	1041	4	US-09-270-767-32619	Sequence 32619, A
846	59	5.4	770	4	US-09-949-016-11360	Sequence 11360, A	919	58.5	5.3	1041	4	US-09-270-767-47836	Sequence 47836, A
847	59	5.4	783	4	US-09-165-396-2	Sequence 2, Appl1	920	58.5	5.3	1054	4	US-09-828-447-11	Sequence 11, Appl
848	59	5.4	830	3	US-08-872-855-11	Sequence 11, Appl	921	58.5	5.3	1198	4	US-09-284-768A-10	Sequence 10, Appl
849	59	5.4	833	1	US-08-264-534-6	Sequence 6, Appl1	922	58.5	5.3	1256	4	US-09-248-796A-18057	Sequence 18057, A
850	59	5.4	833	1	US-08-083-590A-2	Sequence 6, Appl1	923	58.5	5.3	1575	4	US-10-144-198-43	Sequence 43, Appl
851	59	5.4	833	1	US-08-465-500-6	Sequence 6, Appl1	924	58.5	5.3	1584	4	US-10-144-198-24	Sequence 24, Appl
852	59	5.4	833	2	US-08-346-126-6	Sequence 6, Appl1	925	58.5	5.3	2763	3	US-08-496-944-2	Sequence 2, Appl
853	59	5.4	833	2	US-08-346-126-6	Sequence 6, Appl1	926	58.5	5.3	142	4	US-09-513-998C-6264	Sequence 6264, Ap
854	59	5.4	833	3	US-08-532-384-2	Sequence 2, Appl1	927	58.5	5.3	166	4	US-09-270-767-32468	Sequence 32468, A
855	59	5.4	833	3	US-08-893-828-6	Sequence 6, Appl1	928	58.5	5.3	166	4	US-09-270-767-47665	Sequence 47665, A
856	59	5.4	855	4	US-09-107-532A-5646	Sequence 5646, Ap	929	58.5	5.3	219	4	US-09-134-000C-5450	Sequence 5450, Ap
857	59	5.4	876	1	US-08-785-429-2	Sequence 2, Appl1	930	58.5	5.3	239	4	US-09-540-236-3366	Sequence 3366, Ap
858	59	5.4	876	3	US-08-996-621-2	Sequence 2, Appl1	931	58.5	5.3	260	3	US-09-006-353A-8	Sequence 8, Appl1
859	59	5.4	915	4	US-09-107-532A-3714	Sequence 3714, Ap	932	58.5	5.3	260	4	US-09-573-986-8	Sequence 8, Appl1
860	59	5.4	1203	3	US-09-075-272-4	Sequence 4, Appl1	933	58.5	5.3	260	4	US-09-949-016-6047	Sequence 6047, Ap
861	59	5.4	1323	1	US-08-026-138E-4	Sequence 4, Appl1	934	58.5	5.3	272	4	US-09-538-092-551	Sequence 551, App
862	59	5.4	1336	2	US-08-231-193A-58	Sequence 58, Appl	935	58.5	5.3	277	4	US-09-248-796A-21807	Sequence 21807, A
863	59	5.4	1336	2	US-08-486-273A-58	Sequence 58, Appl	936	58.5	5.3	293	4	US-09-252-992A-20791	Sequence 20791, A
864	59	5.4	1336	3	US-08-940-086A-58	Sequence 58, Appl	937	58.5	5.3	293	4	US-09-949-016-7945	Sequence 7945, Ap
865	59	5.4	1336	3	US-08-940-035A-58	Sequence 58, Appl	938	58.5	5.3	301	4	US-09-902-546-12468	Sequence 12468, A
866	59	5.4	1336	3	US-08-935-105A-58	Sequence 58, Appl	939	58.5	5.3	317	4	US-09-252-992A-17668	Sequence 17668, A
867	59	5.4	1336	4	US-09-648-797-58	Sequence 58, Appl	940	58.5	5.3	350	2	US-08-458-970A-9	Sequence 9, Appl1
868	59	5.4	1336	4	US-09-648-123-58	Sequence 58, Appl	941	58.5	5.3	350	4	US-09-107-532A-7070	Sequence 7070, Ap
869	59	5.4	1336	4	US-10-038-937-58	Sequence 58, Appl	942	58.5	5.3	350	4	US-09-826-509-467	Sequence 467, App
870	59	5.4	1445	4	US-09-949-016-11209	Sequence 11209, A	943	58.5	5.3	359	3	US-09-134-001C-5618	Sequence 5618, App
871	59	5.4	2057	4	US-09-499-203-2	Sequence 15, Appl1	944	58.5	5.3	369	3	US-09-117-283-4	Sequence 4, Appl1
872	58.5	5.3	148	3	US-08-540-650B-15	Sequence 15, Appl	945	58.5	5.3	369	4	US-09-812-249-4	Sequence 4, Appl1
873	58.5	5.3	163	4	US-09-198-452A-176	Sequence 176, App	946	58.5	5.3	388	4	US-09-248-796A-18287	Sequence 18287, A
874	58.5	5.3	205	4	US-09-248-796A-16932	Sequence 16932, A	947	58.5	5.3	398	4	US-09-778-510-4	Sequence 4, Appl1
875	58.5	5.3	209	3	US-09-109-100-14	Sequence 14, Appl1	948	58.5	5.3	408	2	US-08-742-440A-5	Sequence 6, Appl1
876	58.5	5.3	212	3	US-09-199-637A-235	Sequence 235, App	949	58.5	5.3	435	4	US-09-489-033A-7287	Sequence 7287, Ap
877	58.5	5.3	218	4	US-09-270-767-44628	Sequence 44628, A	950	58.5	5.3	442	4	US-09-270-767-44598	Sequence 44598, A
878	58.5	5.3	220	4	US-09-248-796A-20150	Sequence 20150, A	951	58.5	5.3	445	5	PCT-US94-05387-7	Sequence 7, Appl1
879	58.5	5.3	237	4	US-09-107-532A-3825	Sequence 3825, Ap	952	58.5	5.3	449	1	US-08-570-157-1	Sequence 1, Appl1
880	58.5	5.3	242	4	US-09-583-110-3522	Sequence 3522, Ap	953	58.5	5.3	449	3	US-09-076-510-1	Sequence 1, Appl1
881	58.5	5.3	262	3	US-09-134-001C-3932	Sequence 3932, Ap	954	58.5	5.3	449	4	US-09-004-349-1	Sequence 1, Appl1
882	58.5	5.3	264	1	US-08-107-042-2	Sequence 2, Appl1	955	58.5	5.3	451	1	US-08-570-157-2	Sequence 2, Appl1
883	58.5	5.3	303	4	US-09-107-532A-6686	Sequence 6686, Ap	956	58.5	5.3	451	3	US-09-076-510-2	Sequence 2, Appl1
884	58.5	5.3	346	4	US-09-215-569B-8	Sequence 8, Appl1	957	58.5	5.3	451	4	US-09-004-349-2	Sequence 2, Appl1
885	58.5	5.3	349	4	US-09-540-236-3199	Sequence 3199, Ap	958	58.5	5.3	452	1	US-07-937-609-16	Sequence 16, Appl
886	58.5	5.3	349	4	US-09-919-497-76	Sequence 76, Appl	959	58.5	5.3	452	3	US-08-029-170-16	Sequence 16, Appl
887	58.5	5.3	352	4	US-09-492-709A-293	Sequence 293, App	960	58.5	5.3	452	4	US-09-443-745-15	Sequence 15, Appl
888	58.5	5.3	352	4	US-09-949-016-11359	Sequence 11359, A	961	58.5	5.3	453	1	US-07-937-608-27	Sequence 27, Appl
889	58.5	5.3	365	4	US-09-899-634C-4	Sequence 4, Appl1	962	58.5	5.3	453	1	US-07-978-892A-5	Sequence 5, Appl1
890	58.5	5.3	367	4	US-09-543-681A-4643	Sequence 4643, Ap	963	58.5	5.3	453	1	US-08-570-157-4	Sequence 4, Appl1
891	58.5	5.3	387	4	US-09-107-532A-5175	Sequence 5175, Ap	964	58.5	5.3	453	3	US-08-029-170-27	Sequence 27, Appl
892	58.5	5.3	407	1	US-08-385-186-15	Sequence 15, Appl	965	58.5	5.3	453	3	US-09-076-510-4	Sequence 4, Appl1
893	58.5	5.3	407	4	US-09-375-252A-14	Sequence 14, Appl	966	58.5	5.3	453	4	US-09-004-349-4	Sequence 4, Appl1
894	58.5	5.3	431	4	US-09-252-991A-27202	Sequence 27202, A	967	58.5	5.3	453	4	US-09-443-745-27	Sequence 27, Appl
895	58.5	5.3	457	4	US-09-248-796A-23295	Sequence 23295, A	968	58.5	5.3	480	4	US-09-540-236-3551	Sequence 3551, Ap
896	58.5	5.3	572	5	PCT-US91-08177-11	Sequence 11, Appl	969	58.5	5.3	561	2	US-08-532-795-2	Sequence 2, Appl1
897	58.5	5.3	572	5	PCT-US91-08177-19	Sequence 19, Appl	970	58.5	5.3	569	2	US-08-532-795-23	Sequence 23, Appl
898	58.5	5.3	574	4	US-09-567-458A-4	Sequence 4, Appl1	971	58.5	5.3	570	2	US-08-532-795-25	Sequence 25, Appl
899	58.5	5.3	594	4	US-09-328-352-5490	Sequence 5490, Ap	972	58.5	5.3	571	2	US-08-532-795-19	Sequence 19, Appl
900	58.5	5.3	602	3	US-09-257-490-15	Sequence 15, Appl	973	58.5	5.3	571	2	US-08-532-795-21	Sequence 21, Appl
901	58.5	5.3	656	4	US-09-248-796A-20237	Sequence 20237, A	974	58.5	5.3	571	2	US-09-538-092-737	Sequence 737, App
902	58.5	5.3	680	3	US-08-947-965-77	Sequence 77, Appl	975	58.5	5.3	571	4	US-08-532-795-27	Sequence 27, Appl
903	58.5	5.3	734	4	US-09-248-796A-16776	Sequence 16776, A	976	58.5	5.3	574	2	US-08-532-795-27	Sequence 27, Appl

977	58	5.3	604	4	US-09-345-473E-17	Sequence 17, Appli	1050	57.5	5.2	402	1	US-08-206-864-4	Sequence 4, Appli
978	58	5.3	614	1	US-08-262-338A-4	Sequence 4, Appli	1051	57.5	5.2	402	1	US-08-278-729A-21	Sequence 8, Appli
979	58	5.3	614	1	US-08-460-114A-4	Sequence 4, Appli	1052	57.5	5.2	402	1	US-08-480-528A-8	Sequence 8, Appli
980	58	5.3	614	3	US-09-347-878-38	Sequence 38, Appli	1053	57.5	5.2	402	1	US-08-479-666-8	Sequence 8, Appli
981	58	5.3	614	4	US-09-133-966A-4	GENERAL INFO	1054	57.5	5.2	402	1	US-08-155-343A-21	Sequence 21, Appli
982	58	5.3	623	3	US-09-233-200-69	Sequence 89, Appli	1055	57.5	5.2	402	1	US-08-406-672-51	Sequence 21, Appli
983	58	5.3	623	3	US-09-233-200-98	Sequence 89, Appli	1056	57.5	5.2	402	1	US-08-643-563A-21	Sequence 21, Appli
984	58	5.3	623	3	US-09-233-197-69	Sequence 89, Appli	1057	57.5	5.2	402	1	US-08-447-570-29	Sequence 29, Appli
985	58	5.3	623	3	US-09-233-197-98	Sequence 89, Appli	1058	57.5	5.2	402	1	US-08-643-763A-21	Sequence 21, Appli
986	58	5.3	623	3	US-09-233-201-68	Sequence 89, Appli	1059	57.5	5.2	402	1	US-08-462-623-21	Sequence 21, Appli
987	58	5.3	623	3	US-09-233-201-98	Sequence 89, Appli	1060	57.5	5.2	402	1	US-08-451-553A-21	Sequence 21, Appli
988	58	5.3	623	4	US-09-233-195-89	Sequence 89, Appli	1061	57.5	5.2	402	2	US-08-459-346-6	Sequence 6, Appli
989	58	5.3	623	4	US-09-233-195-98	Sequence 89, Appli	1062	57.5	5.2	402	2	US-08-445-468A-21	Sequence 21, Appli
990	58	5.3	772	4	US-09-134-000C-6491	Sequence 6491, Ap	1063	57.5	5.2	402	2	US-08-901-200A-8	Sequence 8, Appli
991	58	5.3	802	3	US-09-147-236-4	Sequence 4, Appli	1064	57.5	5.2	402	2	US-08-449-700-29	Sequence 29, Appli
992	58	5.3	802	4	US-09-522-474-4	Sequence 4, Appli	1065	57.5	5.2	402	2	US-08-469-699A-29	Sequence 29, Appli
993	58	5.3	806	3	US-08-549-515-5	Sequence 5, Appli	1066	57.5	5.2	402	2	US-08-461-397A-21	Sequence 21, Appli
994	58	5.3	806	3	US-08-549-515-11	Sequence 11, Appli	1067	57.5	5.2	402	2	US-08-912-088-21	Sequence 21, Appli
995	58	5.3	837	3	US-09-012-710-12	Sequence 12, Appli	1068	57.5	5.2	402	3	US-08-278-730A-21	Sequence 21, Appli
996	58	5.3	837	3	US-09-556-273-12	Sequence 12, Appli	1069	57.5	5.2	402	3	US-08-889-419-6	Sequence 6, Appli
997	58	5.3	873	4	US-09-248-796A-20365	Sequence 20365, A	1070	57.5	5.2	402	3	US-08-445-467-21	Sequence 21, Appli
998	58	5.3	895	1	US-08-123-161A-8	Sequence 8, Appli	1071	57.5	5.2	402	3	US-08-480-515A-21	Sequence 21, Appli
999	58	5.3	895	1	US-08-483-278-8	Sequence 8, Appli	1072	57.5	5.2	402	3	US-09-219-391-8	Sequence 8, Appli
1000	58	5.3	895	4	US-09-949-016-6490	Sequence 6490, Ap	1073	57.5	5.2	402	3	US-09-170-936-21	Sequence 21, Appli
1001	58	5.3	920	4	US-09-949-016-7178	Sequence 7178, Ap	1074	57.5	5.2	402	3	US-08-402-542-6	Sequence 6, Appli
1002	58	5.3	935	4	US-09-134-000C-6493	Sequence 6493, Ap	1075	57.5	5.2	402	3	US-08-461-113-21	Sequence 21, Appli
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1005	58	5.3	1575	4	US-09-917-254-83	Sequence 83, Appli	1078	57.5	5.2	402	4	US-09-148-925C-29	Sequence 29, Appli
1006	58	5.3	1575	4	US-09-949-016-6743	Sequence 6743, Ap	1079	57.5	5.2	402	4	US-08-957-425-29	Sequence 29, Appli
1007	57.5	5.2	74	4	US-09-134-001C-5490	Sequence 5490, Ap	1080	57.5	5.2	402	4	US-08-260-675-21	Sequence 21, Appli
1008	57.5	5.2	78	4	US-09-248-796A-23961	Sequence 23961, A	1081	57.5	5.2	402	5	PCT-US92-01968-21	Sequence 21, Appli
1009	57.5	5.2	128	4	US-09-270-767-57421	Sequence 57421, A	1082	57.5	5.2	402	5	PCT-US93-05446-11	Sequence 11, Appli
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1011	57.5	5.2	134	4	US-09-270-767-34609	Sequence 34609, A	1084	57.5	5.2	402	5	PCT-US93-07190-21	Sequence 21, Appli
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1013	57.5	5.2	155	4	US-09-107-532A-5264	Sequence 5264, Ap	1086	57.5	5.2	402	5	PCT-US93-087421-21	Sequence 21, Appli
1014	57.5	5.2	157	3	US-09-134-001C-3371	Sequence 3371, A	1087	57.5	5.2	402	5	PCT-US93-08808-21	Sequence 21, Appli
1015	57.5	5.2	170	4	US-09-270-767-37641	Sequence 37641, A	1088	57.5	5.2	402	5	PCT-US93-08808-21	Sequence 21, Appli
1016	57.5	5.2	170	4	US-09-270-767-52858	Sequence 52858, A	1089	57.5	5.2	402	5	PCT-US93-10520-8	Sequence 8, Appli
1017	57.5	5.2	188	4	US-09-489-039A-13189	Sequence 13189, A	1090	57.5	5.2	402	5	US-09-949-016-5892	Sequence 9882, Ap
1018	57.5	5.2	200	4	US-09-710-279-2126	Sequence 2126, Ap	1091	57.5	5.2	447	3	US-09-370-253-6	Sequence 6, Appli
1019	57.5	5.2	216	4	US-09-248-796A-25541	Sequence 25541, A	1092	57.5	5.2	447	4	US-10-082-272-2	Sequence 2, Appli
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1024	57.5	5.2	253	4	US-09-902-540-12048	Sequence 12048, A	1097	57.5	5.2	455	4	US-09-438-185A-958	Sequence 958, App
1025	57.5	5.2	259	4	US-09-540-236-2366	Sequence 2366, Ap	1098	57.5	5.2	484	4	US-09-538-092-101	Sequence 101, App
1026	57.5	5.2	269	4	US-09-949-016-6121	Sequence 6121, Ap	1099	57.5	5.2	490	3	US-09-126-420A-16	Sequence 16, Appli
1027	57.5	5.2	276	4	US-09-949-016-7261	Sequence 7261, Ap	1100	57.5	5.2	496	4	US-09-134-000C-5822	Sequence 5822, Ap
1028	57.5	5.2	297	4	US-09-270-767-42154	Sequence 42154, A	1101	57.5	5.2	569	4	US-09-248-796A-20249	Sequence 20249, A
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1030	57.5	5.2	311	3	US-08-911-423-8	Sequence 8, Appli	1103	57.5	5.2	627	2	US-08-700-636-6	Sequence 6, Appli
1031	57.5	5.2	314	3	US-09-355-166-17	Sequence 17, Appli	1104	57.5	5.2	627	3	US-08-467-574-6	Sequence 6, Appli
1032	57.5	5.2	319	3	US-08-630-172-12	Sequence 12, Appli	1105	57.5	5.2	627	3	US-09-217-345-6	Sequence 6, Appli
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1034	57.5	5.2	334	4	US-09-710-279-282	Sequence 282, App	1107	57.5	5.2	684	4	US-09-765-298A-18	Sequence 18, Appli
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1036	57.5	5.2	336	4	US-09-270-767-49141	Sequence 49141, A	1109	57.5	5.2	753	4	US-09-949-016-11393	Sequence 11393, A
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1038	57.5	5.2	341	4	US-09-134-000C-4175	Sequence 4175, Ap	1111	57.5	5.2	812	4	US-09-270-767-57403	Sequence 57403, A
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1040	57.5	5.2	359	4	US-09-270-767-42534	Sequence 42534, A	1113	57.5	5.2	837	2	US-08-474-068A-7	Sequence 7, Appli
1041	57.5	5.2	377	4	US-09-949-016-10067	Sequence 10067, A	1114	57.5	5.2	837	2	US-08-412-481-6	Sequence 6, Appli
1042	57.5	5.2	377	4	US-09-949-016-10068	Sequence 10068, A	1115	57.5	5.2	878	1	US-08-237-919-2	Sequence 2, Appli
1043	57.5	5.2	390	3	US-09-414-010-2	Sequence 2, Appli	1116	57.5	5.2	878	1	US-08-732-429-2	Sequence 2, Appli
1044	57.5	5.2	390	4	US-09-812-216-2	Sequence 2, Appli	1117	57.5	5.2	878	4	US-09-798-267-2	Sequence 2, Appli
1045	57.5	5.2	390	4	US-09-949-016-9665	Sequence 9665, Ap	1118	57.5	5.2	878	4	US-09-798-267-3	Sequence 3, Appli
1046	57.5	5.2	399	5	PCT-US91-07635-6	Sequence 6, Appli	1119	57.5	5.2	878	5	PCT-US95-05518-2	Sequence 2, Appli
1047	57.5	5.2	402	1	US-07-841-646-29	Sequence 29, Appli	1120	57.5	5.2	921	4	US-09-949-016-7787	Sequence 7787, Ap
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1049	57.5	5.2	402	1	US-08-147-023-29	Sequence 29, Appli	1122	57.5	5.2	932	4	US-08-468-024B-4	Sequence 4, Appli

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1124	57.5	5.2	932	4	US-08-465-679-4	Sequence 4, Appl1	1197	57	5.2	427	4	US-09-270-767-45426	Sequence 45426, A
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1126	57.5	5.2	932	4	US-09-788-657-18	Sequence 18, Appl	1199	57	5.2	432	4	US-09-949-016-6467	Sequence 6467, Ap
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1132	57.5	5.2	1228	4	US-09-463-402-2	Sequence 2, Appl1	1205	57	5.2	458	4	US-08-464-258B-3	Sequence 3, Appl1
1133	57.5	5.2	1228	4	US-09-889-572-2	Sequence 2, Appl1	1206	57	5.2	484	3	US-09-328-352-4849	Sequence 4849, Ap
1134	57.5	5.2	1228	4	US-09-117-447-2	Sequence 2, Appl1	1207	57	5.2	517	4	US-09-134-000C-6121	Sequence 6121, Ap
1135	57.5	5.2	1249	4	US-09-538-092-1031	Sequence 1031, Ap	1208	57	5.2	541	4	US-09-248-796A-18318	Sequence 18318, A
1136	57.5	5.2	1249	4	US-09-949-016-6338	Sequence 6338, Ap	1209	57	5.2	574	3	US-09-248-796A-18722	Sequence 18722, A
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1138	57.5	5.2	1319	2	US-08-290-731C-2	Sequence 2, Appl1	1211	57	5.2	669	2	US-08-357-533A-8	Sequence 8, Appl1
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1145	57	5.2	76	4	US-09-134-000C-3740	Sequence 3740, Ap	1218	57	5.2	774	2	US-08-486-273A-42	Sequence 42, Appl
1146	57	5.2	105	4	US-09-710-279-434	Sequence 434, App	1219	57	5.2	774	3	US-08-480-477A-42	Sequence 42, Appl
1147	57	5.2	114	3	US-09-134-001C-5025	Sequence 5025, Ap	1220	57	5.2	774	3	US-08-940-035A-42	Sequence 42, Appl
1148	57	5.2	148	4	US-09-134-000C-5009	Sequence 5009, Ap	1221	57	5.2	774	3	US-08-940-035A-42	Sequence 42, Appl
1149	57	5.2	163	4	US-09-270-767-61961	Sequence 61961, A	1222	57	5.2	774	3	US-08-935-105A-42	Sequence 42, Appl
1150	57	5.2	174	4	US-09-710-279-1550	Sequence 1520, Ap	1223	57	5.2	774	4	US-09-648-797-42	Sequence 42, Appl
1151	57	5.2	208	4	US-09-328-352-5111	Sequence 5111, Ap	1224	57	5.2	774	4	US-09-386-123-42	Sequence 42, Appl
1152	57	5.2	211	3	US-09-075-454-6	Sequence 6, Appl1	1225	57	5.2	774	4	US-10-038-937-42	Sequence 42, Appl
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1154	57	5.2	218	3	US-08-228-208A-19	Sequence 19, Appl	1227	57	5.2	787	1	US-08-268-165A-110	Sequence 110, App
1155	57	5.2	225	1	US-08-505-058-3	Sequence 3, Appl1	1228	57	5.2	787	2	US-08-453-702A-110	Sequence 110, App
1156	57	5.2	225	2	US-08-459-818-23	Sequence 23, Appl	1229	57	5.2	787	3	US-09-099-633-110	Sequence 110, App
1157	57	5.2	225	2	US-08-889-666-23	Sequence 23, Appl	1230	57	5.2	787	5	PCR-US95-08071-110	Sequence 110, App
1158	57	5.2	225	2	US-08-465-078-23	Sequence 23, Appl	1231	57	5.2	952	4	US-09-270-767-41680	Sequence 41680, A
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1160	57	5.2	225	2	US-08-488-062-23	Sequence 23, Appl	1233	57	5.2	1075	1	US-07-623-033-2	Sequence 2, Appl1
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1162	57	5.2	228	3	US-08-911-423-2	Sequence 2, Appl1	1235	57	5.2	1149	4	US-09-949-016-7682	Sequence 7682, Ap
1163	57	5.2	228	4	US-09-512-363-7	Sequence 7, Appl1	1236	57	5.2	1171	4	US-09-949-016-9738	Sequence 9738, Ap
1164	57	5.2	228	4	US-09-176-200-7	Sequence 7, Appl1	1237	57	5.2	1214	2	US-08-231-193A-54	Sequence 54, Appl
1165	57	5.2	228	4	US-09-915-593-7	Sequence 7, Appl1	1238	57	5.2	1214	2	US-08-486-273A-54	Sequence 54, Appl
1166	57	5.2	229	4	US-08-916-442-2	Sequence 2, Appl1	1239	57	5.2	1214	3	US-08-480-477A-54	Sequence 54, Appl
1167	57	5.2	229	4	US-09-731-924A-2	Sequence 2, Appl1	1240	57	5.2	1214	3	US-08-940-086A-54	Sequence 54, Appl
1168	57	5.2	229	4	US-09-317-641-2	Sequence 2, Appl1	1241	57	5.2	1214	3	US-08-940-035A-54	Sequence 54, Appl
1169	57	5.2	236	4	US-09-489-039A-9771	Sequence 9771, Ap	1242	57	5.2	1214	4	US-09-648-797-54	Sequence 54, Appl
1170	57	5.2	263	4	US-09-252-991A-20351	Sequence 20351, A	1243	57	5.2	1214	4	US-09-648-797-54	Sequence 54, Appl
1171	57	5.2	263	4	US-09-248-796A-14400	Sequence 14400, A	1244	57	5.2	1214	4	US-09-386-123-54	Sequence 54, Appl
1172	57	5.2	265	4	US-09-328-352-8071	Sequence 8071, Ap	1245	57	5.2	1214	4	US-10-038-937-54	Sequence 54, Appl
1173	57	5.2	279	3	US-08-339-214-24	Sequence 24, Appl	1246	57	5.2	1219	2	US-08-231-193A-50	Sequence 50, Appl
1174	57	5.2	279	3	US-08-339-214-32	Sequence 32, Appl	1247	57	5.2	1219	2	US-08-486-273A-50	Sequence 50, Appl
1175	57	5.2	279	4	US-09-248-796A-16033	Sequence 16033, A	1248	57	5.2	1219	3	US-08-480-477A-50	Sequence 50, Appl
1176	57	5.2	287	4	US-09-270-767-33263	Sequence 33263, A	1249	57	5.2	1219	3	US-08-940-086A-50	Sequence 50, Appl
1177	57	5.2	287	4	US-09-270-767-48480	Sequence 48480, A	1250	57	5.2	1219	3	US-08-940-035A-50	Sequence 50, Appl
1178	57	5.2	310	4	US-09-252-991A-27339	Sequence 27339, A	1251	57	5.2	1219	3	US-08-935-105A-50	Sequence 50, Appl
1179	57	5.2	330	1	US-08-238-163-2	Sequence 2, Appl1	1252	57	5.2	1219	4	US-09-648-797-50	Sequence 50, Appl
1180	57	5.2	343	4	US-09-489-039A-9368	Sequence 9368, Ap	1253	57	5.2	1219	4	US-09-386-123-50	Sequence 50, Appl
1181	57	5.2	345	2	US-08-332-562A-132	Sequence 132, App	1254	57	5.2	1231	4	US-10-038-937-50	Sequence 50, Appl
1182	57	5.2	352	4	US-09-949-016-6781	Sequence 6781, Ap	1255	57	5.2	1231	2	US-08-231-193A-48	Sequence 48, Appl
1183	57	5.2	361	4	US-09-755-665-57	Sequence 57, Appl	1256	57	5.2	1231	2	US-08-486-273A-48	Sequence 48, Appl
1184	57	5.2	374	4	US-09-949-016-7689	Sequence 7689, Ap	1257	57	5.2	1231	3	US-08-480-477A-48	Sequence 48, Appl
1185	57	5.2	377	3	US-09-410-464-8	Sequence 8, Appl1	1258	57	5.2	1231	3	US-08-940-086A-48	Sequence 48, Appl
1186	57	5.2	379	4	US-09-107-433-4510	Sequence 4510, Ap	1259	57	5.2	1231	3	US-08-940-035A-48	Sequence 48, Appl
1187	57	5.2	382	4	US-09-328-352-4335	Sequence 4335, Ap	1260	57	5.2	1231	3	US-08-935-105A-48	Sequence 48, Appl
1188	57	5.2	397	3	US-08-948-997-5	Sequence 5, Appl1	1261	57	5.2	1231	4	US-09-648-797-48	Sequence 48, Appl
1189	57	5.2	397	3	US-09-348-817A-5	Sequence 5, Appl1	1262	57	5.2	1231	4	US-09-386-123-48	Sequence 48, Appl
1190	57	5.2	397	3	US-09-722-292-5	Sequence 5, Appl1	1263	57	5.2	1231	4	US-10-038-937-48	Sequence 48, Appl
1191	57	5.2	414	4	US-09-755-665-14	Sequence 14, Appl	1264	57	5.2	1236	2	US-08-231-193A-6	Sequence 6, Appl1
1192	57	5.2	414	4	US-09-755-665-55	Sequence 55, Appl	1265	57	5.2	1236	2	US-08-486-273A-6	Sequence 6, Appl1
1193	57	5.2	414	4	US-09-755-665-56	Sequence 56, Appl	1266	57	5.2	1236	3	US-08-480-477A-6	Sequence 6, Appl1
1194	57	5.2	415	4	US-09-461-325-134	Sequence 134, App	1267	57	5.2	1236	3	US-08-940-086A-6	Sequence 6, Appl1
1195	57	5.2	415	4	US-10-012-542-134	Sequence 134, App	1268	57	5.2	1236	3	US-08-940-035A-6	Sequence 6, Appl1



1269	57	5.2	1236	3	US-08-935-105A-6	Sequence 6, Appl1	1342	56.5	5.1	398	4	US-09-461-908-2	Sequence 2, Appl1
1270	57	5.2	1236	4	US-09-648-797-6	Sequence 6, Appl1	1343	56.5	5.1	398	4	US-08-441-893A-2	Sequence 2, Appl1
1271	57	5.2	1236	4	US-09-386-123-6	Sequence 6, Appl1	1344	56.5	5.1	398	4	US-09-579-845-4	Sequence 4, Appl1
1272	57	5.2	1236	4	US-10-038-937-6	Sequence 6, Appl1	1345	56.5	5.1	398	4	US-08-406-824A-8	Sequence 8, Appl1
1273	57	5.2	1239	1	US-08-026-138E-3	Sequence 3, Appl1	1346	56.5	5.1	398	4	US-09-921-667-6	Sequence 2, Appl1
1274	57	5.2	1239	2	US-08-231-193A-52	Sequence 52, Appl1	1347	56.5	5.1	398	5	PCT-US91-03478-2	Sequence 8, Appl1
1275	57	5.2	1239	2	US-08-486-273A-52	Sequence 52, Appl1	1348	56.5	5.1	402	4	US-09-543-681A-6953	Sequence 6953, Ap
1276	57	5.2	1239	3	US-08-486-474-52	Sequence 52, Appl1	1349	56.5	5.1	408	4	US-09-949-016-6513	Sequence 8513, Ap
1277	57	5.2	1239	3	US-08-940-086A-52	Sequence 52, Appl1	1350	56.5	5.1	413	4	US-09-543-681A-5108	Sequence 5108, Ap
1278	57	5.2	1239	3	US-08-940-086A-52	Sequence 52, Appl1	1351	56.5	5.1	418	4	US-09-949-016-9458	Sequence 9458, Ap
1279	57	5.2	1239	3	US-08-935-105A-52	Sequence 52, Appl1	1352	56.5	5.1	445	4	US-09-328-352-4631	Sequence 4631, Ap
1280	57	5.2	1239	4	US-09-648-797-52	Sequence 52, Appl1	1353	56.5	5.1	461	4	US-09-949-016-9508	Sequence 8508, Ap
1281	57	5.2	1239	4	US-09-386-123-52	Sequence 52, Appl1	1354	56.5	5.1	481	4	US-09-902-540-13111	Sequence 13111, A
1282	57	5.2	1239	4	US-10-038-937-52	Sequence 52, Appl1	1355	56.5	5.1	482	4	US-09-328-352-6084	Sequence 6084, Ap
1283	57	5.2	1244	2	US-08-231-193A-46	Sequence 46, Appl1	1356	56.5	5.1	488	4	US-09-248-796A-18644	Sequence 18644, A
1284	57	5.2	1244	2	US-08-486-273A-46	Sequence 46, Appl1	1357	56.5	5.1	490	4	US-09-248-796A-23937	Sequence 23937, A
1285	57	5.2	1244	3	US-08-480-474-46	Sequence 46, Appl1	1358	56.5	5.1	500	3	US-09-292-768-4	Sequence 4, Appl1
1286	57	5.2	1244	3	US-08-940-086A-46	Sequence 46, Appl1	1359	56.5	5.1	500	3	US-09-252-768-68	Sequence 68, Appl1
1287	57	5.2	1244	3	US-08-940-035A-46	Sequence 46, Appl1	1360	56.5	5.1	500	3	US-09-292-768-70	Sequence 70, Appl1
1288	57	5.2	1244	3	US-08-935-105A-46	Sequence 46, Appl1	1361	56.5	5.1	507	4	US-09-328-352-7742	Sequence 7742, Ap
1289	57	5.2	1244	4	US-09-648-797-46	Sequence 46, Appl1	1362	56.5	5.1	522	3	US-09-142-732-2	Sequence 2, Appl1
1290	57	5.2	1244	4	US-09-386-123-46	Sequence 46, Appl1	1363	56.5	5.1	522	4	US-08-945-826-2	Sequence 2, Appl1
1291	57	5.2	1244	4	US-10-038-937-46	Sequence 46, Appl1	1364	56.5	5.1	522	4	US-09-197-503-2	Sequence 2, Appl1
1292	57	5.2	1333	3	US-09-347-878-20	Sequence 20, Appl1	1365	56.5	5.1	522	4	US-07-469-039A-10999	Sequence 10999, A
1293	57	5.2	1333	3	US-09-949-016-7739	Sequence 7739, Ap	1366	56.5	5.1	529	1	US-07-779-890-2	Sequence 2, Appl1
1294	57	5.2	1389	2	US-08-619-198-5	Sequence 5, Appl1	1367	56.5	5.1	529	5	PCT-US93-05640-2	Sequence 2, Appl1
1295	57	5.2	1559	4	US-09-949-016-10190	Sequence 4, Appl1	1368	56.5	5.1	529	5	US-09-647-390-18	Sequence 18, Appl1
1296	57	5.2	1693	4	US-09-560-385A-4	Sequence 8, Appl1	1369	56.5	5.1	540	4	US-09-107-532A-4126	Sequence 4126, Ap
1297	57	5.2	1693	3	US-09-560-385A-8	Sequence 24, Appl1	1370	56.5	5.1	585	4	US-09-107-532A-6918	Sequence 6918, Ap
1298	57	5.2	1713	4	US-08-600-982-24	Sequence 6, Appl1	1371	56.5	5.1	586	4	US-09-107-532A-7027	Sequence 7027, Ap
1299	57	5.2	1713	4	US-09-560-385A-6	Sequence 6, Appl1	1372	56.5	5.1	598	4	US-09-107-532A-7027	Sequence 7027, Ap
1300	57	5.2	1713	4	US-09-538-092-1359	Sequence 1359, Ap	1373	56.5	5.1	627	4	US-09-949-016-9447	Sequence 9447, Ap
1301	57	5.2	1713	5	PCT-US94-10261A-24	Sequence 24, Appl1	1374	56.5	5.1	640	4	US-09-907-794A-292	Sequence 292, App
1302	57	5.2	1724	4	US-09-560-385A-2	Sequence 2, Appl1	1375	56.5	5.1	640	4	US-09-905-125A-292	Sequence 292, App
1303	57	5.2	1780	4	US-09-949-016-6899	Sequence 6899, Ap	1376	56.5	5.1	640	4	US-09-902-775A-292	Sequence 292, App
1304	57	5.2	1786	4	US-09-949-016-7880	Sequence 7880, Ap	1377	56.5	5.1	640	4	US-09-906-700-292	Sequence 292, App
1305	57	5.2	2233	2	US-08-569-853-1	Sequence 1, Appl1	1378	56.5	5.1	640	4	US-09-903-603A-292	Sequence 292, App
1306	57	5.2	2233	2	US-08-987-439-1	Sequence 1, Appl1	1379	56.5	5.1	640	4	US-09-904-920A-292	Sequence 292, App
1307	57	5.2	5032	4	US-09-538-092-979	Sequence 979, App	1380	56.5	5.1	640	4	US-09-909-064-292	Sequence 292, App
1308	57	5.2	5037	4	US-09-424-783-4	Sequence 4, Appl1	1381	56.5	5.1	640	4	US-09-905-381A-292	Sequence 292, App
1309	56.5	5.1	1332	4	US-09-710-279-734	Sequence 734, App	1382	56.5	5.1	640	4	US-08-966-618-292	Sequence 292, App
1310	56.5	5.1	1339	4	US-09-270-767-47859	Sequence 47859, A	1383	56.5	5.1	649	1	US-08-477-476-2	Sequence 2, Appl1
1311	56.5	5.1	150	4	US-09-949-016-6171	Sequence 6171, Ap	1384	56.5	5.1	649	2	PCT-US96-07354-2	Sequence 2, Appl1
1312	56.5	5.1	160	4	US-09-710-279-3144	Sequence 3144, Ap	1385	56.5	5.1	649	5	US-09-949-016-10883	Sequence 10883, A
1313	56.5	5.1	163	5	PCT-US91-02942-5	Sequence 5, Appl1	1386	56.5	5.1	650	3	US-09-310-463-2	Sequence 2, Appl1
1314	56.5	5.1	170	4	US-09-198-452A-191	Sequence 191, App	1387	56.5	5.1	650	4	US-08-842-248A-2	Sequence 2, Appl1
1315	56.5	5.1	170	4	US-09-438-185A-176	Sequence 176, App	1388	56.5	5.1	651	3	US-08-985-950-22	Sequence 22, Appl1
1316	56.5	5.1	177	4	US-09-270-767-43412	Sequence 43412, A	1389	56.5	5.1	651	4	US-09-546-049-22	Sequence 22, Appl1
1317	56.5	5.1	194	4	US-09-640-211A-802	Sequence 802, App	1390	56.5	5.1	664	4	US-09-823-038A-48	Sequence 48, Appl1
1318	56.5	5.1	252	4	US-09-252-991A-17553	Sequence 17553, A	1391	56.5	5.1	664	4	US-09-902-540-12181	Sequence 12181, A
1319	56.5	5.1	254	4	US-09-543-681A-7333	Sequence 7333, Ap	1392	56.5	5.1	667	4	US-09-949-016-10883	Sequence 10883, A
1320	56.5	5.1	284	1	US-08-390-8588B-36	Sequence 36, Appl1	1393	56.5	5.1	729	4	US-09-543-681A-8257	Sequence 8257, Ap
1321	56.5	5.1	290	4	US-09-252-991A-25306	Sequence 25306, A	1394	56.5	5.1	732	4	US-09-270-767-18665	Sequence 38665, A
1322	56.5	5.1	300	3	US-08-935-165A-386	Sequence 386, App	1395	56.5	5.1	732	4	US-09-270-767-53882	Sequence 53882, A
1323	56.5	5.1	309	4	US-09-248-796A-15871	Sequence 15871, A	1396	56.5	5.1	761	4	US-09-949-016-6880	Sequence 6880, Ap
1324	56.5	5.1	327	2	US-08-651-818A-3	Sequence 3, Appl1	1397	56.5	5.1	771	4	US-09-902-540-12980	Sequence 12980, A
1325	56.5	5.1	327	4	US-09-184-826-3	Sequence 3, Appl1	1398	56.5	5.1	851	4	US-09-949-016-7187	Sequence 7187, Ap
1326	56.5	5.1	327	4	US-09-832-464-3	Sequence 3, Appl1	1399	56.5	5.1	851	4	US-09-619-353-12	Sequence 12, Appl1
1327	56.5	5.1	338	3	US-09-134-001C-5155	Sequence 5155, Ap	1400	56.5	5.1	916	1	US-08-188-228-48	Sequence 48, Appl1
1328	56.5	5.1	359	2	US-08-103-170-7	Sequence 74, Appl1	1401	56.5	5.1	916	1	US-08-332-643-42	Sequence 42, Appl1
1329	56.5	5.1	363	4	US-09-491-577-74	Sequence 74, Appl1	1402	56.5	5.1	916	1	US-08-332-638-48	Sequence 48, Appl1
1330	56.5	5.1	366	4	US-08-489-039A-7522	Sequence 7522, Ap	1403	56.5	5.1	929	4	US-09-949-016-11143	Sequence 11143, A
1331	56.5	5.1	373	2	US-08-599-171A-26	Sequence 26, Appl1	1404	56.5	5.1	1004	4	US-09-248-796A-18119	Sequence 18119, A
1332	56.5	5.1	373	3	US-08-646-590B-26	Sequence 26, Appl1	1405	56.5	5.1	1051	3	US-08-966-762-14	Sequence 14, Appl1
1333	56.5	5.1	373	3	US-09-069-226-26	Sequence 26, Appl1	1406	56.5	5.1	1051	4	US-09-911-927-14	Sequence 14, Appl1
1334	56.5	5.1	373	3	US-09-412-184-26	Sequence 26, Appl1	1407	56.5	5.1	1051	4	US-09-911-882-14	Sequence 14, Appl1
1335	56.5	5.1	376	4	US-09-949-016-6504	Sequence 6504, Ap	1408	56.5	5.1	1051	4	US-09-911-888-14	Sequence 14, Appl1
1336	56.5	5.1	393	1	US-08-499-568-15	Sequence 15, Appl1	1409	56.5	5.1	1090	3	US-08-307-896-3	Sequence 3, Appl1
1337	56.5	5.1	393	2	US-08-793-958-15	Sequence 15, Appl1	1410	56.5	5.1	1090	3	US-08-726-214-4	Sequence 4, Appl1
1338	56.5	5.1	393	2	US-08-956-998-2	Sequence 2, Appl1	1411	56.5	5.1	1090	4	US-09-245-039-3	Sequence 3, Appl1
1339	56.5	5.1	398	1	US-08-091-519-2	Sequence 2, Appl1	1412	56.5	5.1	1090	5	PCT-US95-11808-3	Sequence 3, Appl1
1340	56.5	5.1	398	1	US-08-442-043A-2	Sequence 2, Appl1	1413	56.5	5.1	1972	5	US-09-418-710-21	Sequence 21, Appl1
1341	56.5	5.1	398	3	US-09-173-151A-26	Sequence 26, Appl1	1414	56.5	5.1	1972	4	US-09-839-479-21	Sequence 21, Appl1



1415	56.5	5.1	2304	3	US-09-324-867-4	Sequence 4, Appl1
1416	56.5	5.1	2733	4	US-09-949-016-11433	Sequence 11433, A
1417	56.5	5.1	3259	4	US-09-949-016-6507	Sequence 6507, Ap
1418	56	5.1	125	4	US-09-248-796A-16431	Sequence 16431, A
1419	56	5.1	137	4	US-09-513-999C-7963	Sequence 7963, Ap
1420	56	5.1	138	4	US-09-647-468-167	Sequence 167, Ap
1421	56	5.1	140	4	US-10-101-464A-530	Sequence 530, App
1422	56	5.1	146	4	US-09-582-337-10	Sequence 10, Appl
1423	56	5.1	155	4	US-09-270-767-60154	Sequence 60154, A
1424	56	5.1	166	4	US-09-621-976-4280	Sequence 4280, Ap
1425	56	5.1	168	4	US-09-949-016-8494	Sequence 8494, Ap
1426	56	5.1	169	4	US-09-543-681A-4307	Sequence 4307, Ap
1427	56	5.1	222	4	US-09-902-540-11510	Sequence 11510, A
1428	56	5.1	229	3	US-09-134-001C-4241	Sequence 4241, Ap
1429	56	5.1	243	4	US-09-248-796A-16807	Sequence 16807, A
1430	56	5.1	247	4	US-09-328-352-6638	Sequence 6638, Ap
1431	56	5.1	256	4	US-09-489-039A-11853	Sequence 11853, A
1432	56	5.1	257	4	US-09-205-258-421	Sequence 421, App
1433	56	5.1	261	4	US-09-540-236-2122	Sequence 2122, Ap
1434	56	5.1	272	4	US-09-489-039A-10410	Sequence 10410, A
1435	56	5.1	277	4	US-09-270-767-46151	Sequence 46151, A
1436	56	5.1	286	4	US-09-949-016-6318	Sequence 6318, Ap
1437	56	5.1	300	4	US-09-270-767-44700	Sequence 44700, A
1438	56	5.1	302	4	US-09-489-039A-12820	Sequence 12820, A
1439	56	5.1	302	4	US-09-134-000C-5216	Sequence 5216, Ap
1440	56	5.1	325	1	US-08-142-473A-9	Sequence 9, Appl1
1441	56	5.1	325	1	US-08-469-203A-9	Sequence 9, Appl1
1442	56	5.1	325	1	US-08-469-203A-9	Sequence 9, Appl1
1443	56	5.1	334	4	US-09-710-279-230	Sequence 230, App
1444	56	5.1	337	3	US-09-331-581-24	Sequence 24, Appl
1445	56	5.1	345	4	US-09-248-796A-20049	Sequence 20049, A
1446	56	5.1	351	4	US-09-489-039A-7442	Sequence 7442, Ap
1447	56	5.1	355	2	US-08-666-367B-6	Sequence 6, Appl1
1448	56	5.1	355	3	US-09-143-438-6	Sequence 6, Appl1
1449	56	5.1	356	4	US-09-270-767-46120	Sequence 46120, A
1450	56	5.1	369	4	US-09-489-039A-9526	Sequence 9526, Ap
1451	56	5.1	372	4	US-09-949-016-7605	Sequence 7605, Ap
1452	56	5.1	384	3	US-09-134-001C-4201	Sequence 4201, Ap
1453	56	5.1	385	2	US-08-605-106-14	Sequence 14, Appl
1454	56	5.1	391	4	US-09-721-870-38	Sequence 38, Appl
1455	56	5.1	393	3	US-08-900-230-5	Sequence 5, Appl1
1456	56	5.1	398	4	US-09-778-510-6	Sequence 6, Appl1
1457	56	5.1	398	4	US-09-907-794A-84	Sequence 84, Appl
1458	56	5.1	398	4	US-09-905-125A-84	Sequence 84, Appl
1459	56	5.1	398	4	US-09-902-775A-84	Sequence 84, Appl
1460	56	5.1	398	4	US-09-906-700-84	Sequence 84, Appl
1461	56	5.1	398	4	US-09-903-603A-84	Sequence 84, Appl
1462	56	5.1	398	4	US-09-904-920A-84	Sequence 84, Appl
1463	56	5.1	398	4	US-09-909-064-84	Sequence 84, Appl
1464	56	5.1	398	4	US-09-905-381A-84	Sequence 84, Appl
1465	56	5.1	398	4	US-09-906-618-84	Sequence 84, Appl
1466	56	5.1	403	4	US-10-140-372-2	Sequence 2, Appl1
1467	56	5.1	403	4	US-09-796-487-7	Sequence 7, Appl1
1468	56	5.1	404	3	US-09-134-001C-4261	Sequence 4261, Ap
1469	56	5.1	409	1	US-08-440-103-21	Sequence 21, Appl
1470	56	5.1	409	1	US-08-440-103-24	Sequence 24, Appl
1471	56	5.1	409	1	US-08-440-542-21	Sequence 21, Appl
1472	56	5.1	409	1	US-08-440-542-24	Sequence 24, Appl
1473	56	5.1	409	1	US-08-231-368-21	Sequence 21, Appl
1474	56	5.1	409	1	US-08-231-368-24	Sequence 24, Appl
1475	56	5.1	409	1	US-08-440-210-21	Sequence 21, Appl
1476	56	5.1	409	1	US-08-440-210-24	Sequence 24, Appl
1477	56	5.1	409	3	US-09-046-604-21	Sequence 21, Appl
1478	56	5.1	409	3	US-09-046-604-24	Sequence 24, Appl
1479	56	5.1	418	4	US-09-489-039A-12883	Sequence 12883, A
1480	56	5.1	432	4	US-09-778-510-2	Sequence 2, Appl1
1481	56	5.1	461	4	US-09-248-796A-23597	Sequence 23597, A
1482	56	5.1	467	4	US-09-248-796A-16430	Sequence 16430, A
1483	56	5.1	469	4	US-09-328-352-4250	Sequence 4250, Ap
1484	56	5.1	471	4	US-09-543-681A-7497	Sequence 7497, Ap
1485	56	5.1	491	4	US-09-248-796A-22333	Sequence 22333, A
1486	56	5.1	499	4	US-09-134-000C-6069	Sequence 6069, Ap
1487	56	5.1	508	4	US-09-328-352-6467	Sequence 6467, Ap

1488	56	5.1	519	4	US-09-107-532A-6778	Sequence 6778, Ap
1489	56	5.1	524	4	US-09-252-991A-18092	Sequence 18092, A
1490	56	5.1	558	4	US-09-949-016-8851	Sequence 8851, Ap
1491	56	5.1	594	3	US-08-867-611-48	Sequence 48, Appl
1492	56	5.1	594	4	US-09-690-359-48	Sequence 48, Appl
1493	56	5.1	599	3	US-08-867-611-18	Sequence 18, Appl
1494	56	5.1	599	4	US-09-690-359-18	Sequence 18, Appl
1495	56	5.1	599	5	PCT-US92-06965A-23	Sequence 23, Appl
1496	56	5.1	623	4	US-09-949-016-11206	Sequence 11206, A
1497	56	5.1	646	4	US-09-949-016-6728	Sequence 6728, Ap
1498	56	5.1	646	4	US-09-653-961-2	Sequence 2, Appl1
1499	56	5.1	646	4	US-09-653-961-4	Sequence 4, Appl1
1500	56	5.1	651	4	US-09-949-016-8426	Sequence 8426, Ap

ALIGNMENTS

RESULT 1

US-08-989-299-2

Sequence 2, Application US/08989299

Patent No. 6194356

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

APPLICANT: Robinson, Keith E.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG

TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HONG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,299

FILING DATE: 11-DEC-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Arnold E., Beth

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET INFORMATION: MIA-025.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 805 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-989-299-2

Query Match

Best Local Similarity 34.1%; Score 376; DB 3; Length 805;

Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY	19	PAENAFKRRISIRALDGKAYAWTNEEYLFKAMVATSMR---KVPRENT-EISNVL	73
DB	612	PVADSIIVKIRSLKALDQKAYEMNDNEMYFRSSVAYAMQYFLKVKQOMILFGEEDVR	671
QY	74	LCNVQRVSFWFVVDPSK-NHTLPVAVEVOSAIRNKKRINNAPFLINDOTLEFLKIPSTL	132
DB	672	VANLPRISFNFPVAPKQVSIITRTVEKAIIRMSRRLINDAPFLNDSLEFLGIQFTL	731
QY	133	APPMDPSVPIWIIIFGVIFCIIVALLISGIWQRRKNKEPS	177

Db 732 GPNQPPVSIWLVGVGMVIVGIVILLFTGIRDRKKKKARS 776

RESULT 2

US-10-158-847-142

Sequence 142, Application US/10158847

Patent No. 6592865

GENERAL INFORMATION:

APPLICANT: Tom Parry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

FILE REFERENCE: P5557

CURRENT APPLICATION NUMBER: US/10/158, 847

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: 60/295,004

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SOFTWARE: Patentin version 3.1

SEQ ID NO 142

LENGTH: 805

TYPE: PRT

ORGANISM: homo sapiens

US-10-158-847-142

Query Match 34.1%; Score 376; DB 4; Length 805;

Best Local Similarity 47.9%; Pred. No. 2.5e-34;

Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

Qy 19 PGAENAFKRLSIRLTALGDKAYAMDNTNEEYLFKAMVAFSMR---KVPNREAT-EISHVL 73

Db 612 PYADQSIKVRISLKSALGDKAYEMWNDNEMYLFRSSVAYAMQYFLKYNQWILFGEEEDVR 671

Qy 74 LCNVTORVSFWFVVTDPESK-NHTLPAVEVQSAIRNKKRINNAFPLNDQTEFLKIPSTL 132

Db 672 VANLKPRISFNFVYAPKNSVDIIPRTEVEKAIKMSRSRINDAPLNDNSLEFLGIQPTL 731

Qy 133 APPMDPSVPIWIIIFGVIFCIIIVAILLLISGIMQRRKKKEPS 177

Db 732 GPNQPPVSIWLVGVGMVIVGIVILLFTGIRDRKKKKARS 776

RESULT 3

US-09-407-427-2

Sequence 2, Application US/09407427

Patent No. 6610497

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC

TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR

FILE REFERENCE: NMI-132CP2

CURRENT APPLICATION NUMBER: US/09/407,427

CURRENT FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 09/163,648

PRIOR FILING DATE: 1998-09-30

PRIOR APPLICATION NUMBER: 08/989,299

PRIOR FILING DATE: 1997-12-11

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 805

TYPE: PRT

ORGANISM: Homo sapiens

US-09-407-427-2

Query Match 34.1%; Score 376; DB 4; Length 805;

Best Local Similarity 47.9%; Pred. No. 2.5e-34;

Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

Qy 19 PGAENAFKRLSIRLTALGDKAYAMDNTNEEYLFKAMVAFSMR---KVPNREAT-EISHVL 73

Db 612 PYADQSIKVRISLKSALGDKAYEMWNDNEMYLFRSSVAYAMQYFLKYNQWILFGEEEDVR 671

Qy 74 LCNVTORVSFWFVVTDPESK-NHTLPAVEVQSAIRNKKRINNAFPLNDQTEFLKIPSTL 132

Db 672 VANLKPRISFNFVYAPKNSVDIIPRTEVEKAIKMSRSRINDAPLNDNSLEFLGIQPTL 731

Qy 133 APPMDPSVPIWIIIFGVIFCIIIVAILLLISGIMQRRKKKEPS 177

Db 732 GPNQPPVSIWLVGVGMVIVGIVILLFTGIRDRKKKKARS 776

RESULT 4

US-09-949-016-11284

Sequence 11284, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11284

LENGTH: 819

TYPE: PRT

ORGANISM: Human

US-09-949-016-11284

Query Match 34.1%; Score 376; DB 4; Length 819;

Best Local Similarity 47.9%; Pred. No. 2.5e-34;

Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

Qy 19 PGAENAFKRLSIRLTALGDKAYAMDNTNEEYLFKAMVAFSMR---KVPNREAT-EISHVL 73

Db 626 PYADQSIKVRISLKSALGDKAYEMWNDNEMYLFRSSVAYAMQYFLKYNQWILFGEEEDVR 685

Qy 74 LCNVTORVSFWFVVTDPESK-NHTLPAVEVQSAIRNKKRINNAFPLNDQTEFLKIPSTL 132

Db 686 VANLKPRISFNFVYAPKNSVDIIPRTEVEKAIKMSRSRINDAPLNDNSLEFLGIQPTL 745

Qy 133 APPMDPSVPIWIIIFGVIFCIIIVAILLLISGIMQRRKKKEPS 177

Db 746 GPNQPPVSIWLVGVGMVIVGIVILLFTGIRDRKKKKARS 790

RESULT 5

US-10-158-847-138

Sequence 138, Application US/10158847

Patent No. 6592865

GENERAL INFORMATION:

APPLICANT: Tom Parry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

FILE REFERENCE: P5557

CURRENT APPLICATION NUMBER: US/10/158, 847

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: 60/295,004

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SOFTWARE: Patentin version 3.1

SEQ ID NO 138

LENGTH: 711

TYPE: PRT

ORGANISM: homo sapiens

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (219)..(219)

OTHER INFORMATION: Xaa equals any amino acid

NAME/KEY: MISC FEATURE  
LOCATION: (240)..(240)  
OTHER INFORMATION: Xaa equals any amino acid  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (499)..(499)  
OTHER INFORMATION: Xaa equals any amino acid  
US-10-158-847-138

Query Match 32.6%; Score 359; DB 4; Length 711;  
Best Local Similarity 47.2%; Pred. No. 1.9e-32;  
Matches 75; Conservative 32; Mismatches 46; Indels 6; Gaps 3;

QY 19 PGAEAFKRLSIRALGDKAYAMDTNEEYLFKAMVAFSMT---KVPKREAT-EISHTL 73  
DB 551 PYADOSIKRISLTKALGDKAYEMNDNEMYLFRSSVAVAMROYFLKVKQOMILFGEEDVR 610  
QY 74 LCNVQVSVFVWVTDPSK-NHTLPAVEYQSAIRMNKRNINNAFFINDOTLEFLKIPSTL 132  
DB 611 VANLPRISFNFPVAPKPVSDIIRTEVEKAIKRSRINDAFRLNDSLEFLGIQPTL 670  
QY 133 APPMDPSVPIWIIIFGVIFCIIVAILLISGIWQRR 171  
DB 671 GPPNPQPVSIWLVFGVGVVIVGVIVLIFGTGRDKK 709

RESULT 6  
US-10-158-847-140  
Sequence 140, Application US/10158847  
Patent No. 6592865

GENERAL INFORMATION:

APPLICANT: Tom Parry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

FILE REFERENCE: PF557

CURRENT APPLICATION NUMBER: US/10/158,847

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: 60/295,004

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SOFTWARE: PatentIn version 3.1

SEQ ID NO 140

LENGTH: 681

TYPE: PRT

ORGANISM: homo sapiens

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (219)..(219)

OTHER INFORMATION: Xaa equals any amino acid

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (499)..(499)

OTHER INFORMATION: Xaa equals any amino acid

US-10-158-847-140

Query Match 26.2%; Score 289; DB 4; Length 681;  
Best Local Similarity 48.1%; Pred. No. 2.2e-24;  
Matches 63; Conservative 23; Mismatches 39; Indels 6; Gaps 3;

QY 19 PGAEAFKRLSIRALGDKAYAMDTNEEYLFKAMVAFSMT---KVPKREAT-EISHTL 73  
DB 551 PYADOSIKRISLTKALGDKAYEMNDNEMYLFRSSVAVAMROYFLKVKQOMILFGEEDVR 610  
QY 74 LCNVQVSVFVWVTDPSK-NHTLPAVEYQSAIRMNKRNINNAFFINDOTLEFLKIPSTL 132  
DB 611 VANLPRISFNFPVAPKPVSDIIRTEVEKAIKRSRINDAFRLNDSLEFLGIQPTL 670  
QY 133 APPMDPSVPIW 143  
DB 671 GPPNPQPVSIW 681

RESULT 7  
US-08-188-228-42

Sequence 42, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,460

FILING DATE: 19 APR 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5597725and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 799 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-188-228-42

Query Match 8.2%; Score 90; DB 1; Length 799;  
Best Local Similarity 21.4%; Pred. No. 0.28;  
Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAEICPGAEAFKRLSIRALGDKAYAMDTNEEYLFKAMVAFSMTKYPN 63  
DB 432 HTDLERQININADDSKITLAPDLBELSVNINISIAIEIRNHSISVPAIKVLDV-N 490  
QY 64 REATEIS---HYLLC-----NTQVSVFVWVTDPSKNH---TLPAVEYQSAIRMNK 109  
DB 491 DNAPFASEYEAFLENGKPGQVIGTVA-MDKDPKNGHFLYSILPEMVNPNFTIKK 549  
QY 110 NRINNAFPL-----NDQTEFLKIPSTLA---PMPDPSVPIWIIIG----- 148  
DB 550 NEDNSLILAKHNGFNKQEVYLLPIYISGPNLSTSTLTIRVCGCSNDGVQVQCN 609  
QY 149 -----VIFCIIVAILLISGIWQRRKKEPSEVDADKCEMMIT 191  
DB 610 VEAYVLPGLSGALIALIACIILLIVVLF--VTLRRHNG-ELLIKDEDEVRENTIR 666  
QY 192 IEN 194  
DB 667 YDD 669

## RESULT 8

```

US-08-332-638-42
: Sequence 42, Application US/08332638
: Patent No. 5646250
: GENERAL INFORMATION:
: APPLICANT: Suzuki, Shintaro
: TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Borun
: STREET: 6300 Sears Tower, 233 S. Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/332.638
: FILING DATE: 01-NOV-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/872,643
: FILING DATE: 17 APR 1992
: APPLICATION NUMBER: US/08/049,460
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5646250and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31340
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 799 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-332-638-42

```

US-08-188-228-54

```

: Sequence 54 Application US/08188228
: Patent No. 5597725
: GENERAL INFORMATION:
: APPLICANT: Suzuki, Shintaro
: TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Borun
: STREET: 6300 Sears Tower, 233 S. Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent'n Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/188,228
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/049,460
: FILING DATE: 19 APR 1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/872,643
: FILING DATE: 17 APR 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 559772sand, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31340
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 54:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 793 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-188-228-54

```

```

; Sequence 48, Application US/08332643
; Patent No. 5639634
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,643
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,643
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5639634and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-643-48

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. No. 0.32;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

QY 13 HAEICQPGAEVNAFKVRLSIRTLGDKAYAWDT-----NEEYLFKAMVAFSRRKVPN 63
DB 425 HTDLERQFNINADDKITLPLDLRELSVMHNITIIATEIRHQSISRVPVAKVLDV-N 483
QY 64 REATIS---HYLLC-----NVTQRVSFVVTDPDSKNH-----TLPAVEVQSAIRNKK 109
DB 484 DNAPEFASVEYEAFLCENKPGQVIOVSA-MDKDPPKNGHYFLVSLPEMNNPNFTIKK 542
QY 110 NRINNAFL-----NDOTLEFLKIPSTLA-----PPMDSPVPIWIIIFG----- 148
DB 543 NEDNLSLILAKNGNFRQKQEVYLLPIIISDSGNPLSLSTLTITRVCCSNDGVQSCN 602
QY 149 -----VIFCIIVALLILSGIMQRRKKNKSESEVDADCKENMIT 191
DB 603 VEAYVLPGLSMGALIALIACIIILLVIVLF--VTLRRHQKNEPLIIKDDDEVENIIR 660
QY 192 IEN 194
DB 661 YDD 663

```

```

RESULT 11
US-08-332-638-54
; Sequence 54, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:

```

```

; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-638-54

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. No. 0.32;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

QY 13 HAEICQPGAEVNAFKVRLSIRTLGDKAYAWDT-----NEEYLFKAMVAFSRRKVPN 63
DB 425 HTDLERQFNINADDKITLPLDLRELSVMHNITIIATEIRHQSISRVPVAKVLDV-N 483
QY 64 REATIS---HYLLC-----NVTQRVSFVVTDPDSKNH-----TLPAVEVQSAIRNKK 109
DB 484 DNAPEFASVEYEAFLCENKPGQVIOVSA-MDKDPPKNGHYFLVSLPEMNNPNFTIKK 542
QY 110 NRINNAFL-----NDOTLEFLKIPSTLA-----PPMDSPVPIWIIIFG----- 148
DB 543 NEDNLSLILAKNGNFRQKQEVYLLPIIISDSGNPLSLSTLTITRVCCSNDGVQSCN 602
QY 149 -----VIFCIIVALLILSGIMQRRKKNKSESEVDADCKENMIT 191
DB 603 VEAYVLPGLSMGALIALIACIIILLVIVLF--VTLRRHQKNEPLIIKDDDEVENIIR 660
QY 192 IEN 194
DB 661 YDD 663

```

```

RESULT 12
US-09-949-016-7423
; Sequence 7423, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7423  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7423

Query Match 8.1%; Score 89; DB 4; Length 715;  
Best Local Similarity 21.4%; Pred. No. 0.31;  
Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAEICQCAENAFKRLSIRFALGDKAYAMDT-----NEEYLFKAMVAFGMRKYPN 63  
DB HTDLERQFNINADGKITLATPLDRSLSVNHTIATEIRNHSQISRPVPAIKVLDV-N 406  
QY 64 REATEIS--HVLIC-----NTQKVSFWFVVTDPSSKNH-----TLPVAVQSAIRMNK 109  
DB DNAPEFASVEYAFICENGKPGQVIGYUSA-MDKDDPKNGHFLVSLPEMANNRFTTKK 465  
QY 110 NRINNAPFL-----NQGLEFLKIPSTLA---PPMDPSVPWITIIIFG----- 148  
DB 466 NEDNSLSILAHNGFNROKQEVYLPRIISDSGNPPLSTSTLTRVCGSNDGVQSCN 525  
QY 149 -----VIFCIIVAILLSLGMQRRKNKRSSEVDDAEDKCNMT 191  
DB 526 VEAVVPLIGSMGALIALIACILLLVIVLF--VTLRRHN-EPILIKDEDEVENITR 582  
QY 192 IEN 194  
DB 583 YDD 585

RESULT 13  
US-07-946-497-7  
Sequence 7, Application US/07946497  
Patent No. 5506119  
GENERAL INFORMATION:  
APPLICANT: HERRLICH, Peter  
APPLICANT: PONTA, Helmut  
APPLICANT: GUENTHERT, Ursula  
APPLICANT: MATZKU, Siegfried  
APPLICANT: WENZL, Achim  
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA  
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,  
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/946,497  
FILING DATE: 19921109  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16915/145  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: mCD44  
US-07-946-497-7

Query Match 8.0%; Score 88; DB 1; Length 363;  
Best Local Similarity 21.6%; Pred. No. 0.15;  
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPWITIIIFGVIFCIIVAILLSLGMQRR-----PLDKGCI 207  
DB 256 VTTISGPMRRPQIREWLI---LASLALAILAVCIAVNRRRCGQKKUVINGNGTV 312  
QY 172 KNKEPSEVDDAEDKCNMTIENGIPSD----- 171  
DB 313 EDRKPEILNGASKSQEWVHLVKNKEPSETPDQCTADETRNLQSDMKIGV 363

RESULT 14  
US-08-483-322-7  
Sequence 7, Application US/08483322  
Patent No. 5760178  
GENERAL INFORMATION:  
APPLICANT: HERRLICH, Peter  
APPLICANT: PONTA, Helmut  
APPLICANT: GUENTHERT, Ursula  
APPLICANT: MATZKU, Siegfried  
APPLICANT: WENZL, Achim  
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA  
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,  
TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,322  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,497  
FILING DATE: 09-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16915/145  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: mCD44  
US-08-483-322-7

## Query Match

8.0%; Score 88; DB 1; Length 363;  
Best Local Similarity 21.6%; Pred. No. 0.15;

Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLISGMORR-----171  
DB 256 VTTTSGPMRRPQIPFWLI---LASLALALILAVCIANVSRRCQKKLVINGNGTV 312  
QY 172 KKKRSEVDDADCKCENMTIENGIPSD-----FLDMKGI 207  
DB 313 EDRKPSSEINGASKSQEMVHLVKNKPSSETPDQCMTADETRNIQSVDMKIGV 363

## RESULT 15

US-08-478-882-7  
Sequence 7, Application US/08478882

Patent No. 588575

GENERAL INFORMATION:

APPLICANT: HERRLICH, Peter

APPLICANT: PONTA, Helmut

APPLICANT: GUENTHER, Ursula

APPLICANT: MATZKU, Siegfried

APPLICANT: WENZL, Achim

TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA

TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,

TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,882

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/946,497

FILING DATE: 19921109

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16915/145

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 363 amino acids

TYPE: amino acid

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: mCD44

US-08-478-882-7

Query Match 8.0%; Score 88; DB 2; Length 363;  
Best Local Similarity 21.6%; Pred. No. 0.15;

Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLISGMORR-----171  
DB 256 VTTTSGPMRRPQIPFWLI---LASLALALILAVCIANVSRRCQKKLVINGNGTV 312  
QY 172 KKKRSEVDDADCKCENMTIENGIPSD-----FLDMKGI 207  
DB 313 EDRKPSSEINGASKSQEMVHLVKNKPSSETPDQCMTADETRNIQSVDMKIGV 363

DB 256 VTTTSGPMRRPQIPFWLI---LASLALALILAVCIANVSRRCQKKLVINGNGTV 312

QY 172 KKKRSEVDDADCKCENMTIENGIPSD-----FLDMKGI 207

DB 313 EDRKPSSEINGASKSQEMVHLVKNKPSSETPDQCMTADETRNIQSVDMKIGV 363

Search completed: August 18, 2005, 17:33:46  
Job time : 43 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2005, 17:31:04 ; Search time 172 Seconds

(without alignments)  
631.167 Million cell updates/sec

Title: US-09-997-641-387

perfect score: 1102  
Sequence: 1 MMLLFLVLTATIAHLELCPG.....ENGIPSDPLDMKGLIMPSP 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt\_Q3:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1102	100.0	212	06UM07	06um07 homo sapien
2	1073	97.4	222	09HBJ8	09hbj8 homo sapien
3	935	84.8	222	06AYY2	06ayy2 ractus norv
4	928	84.2	222	09ESG4	09esg4 mus musculu
5	921	83.6	222	09ESG3	09esg3 ractus norv
6	488	44.3	228	06PE94	06pe94 xenopus lae
7	405	36.8	235	06P0S0	06p0s0 brachydanto
8	376	34.1	804	09UPZ6	09upz6 homo sapien
9	376	34.1	805	09WRA7	09wra7 homo sapien
10	376	34.1	816	09BWT0	09bwt0 homo sapien
11	373	33.8	805	09BYF1	09byf1 homo sapien
12	361	32.8	805	09RO10	09ro10 mus musculu
13	357	32.4	265	09D836	09d836 mus musculu
14	357	32.4	265	09D836	09d836 mus musculu
15	100	9.1	1053	08TRA08	08tra08 plasmodium
16	97.5	8.8	1086	018428	018428 geodia cydo
17	96.5	8.8	543	08C0H7	08c0h7 mus musculu
18	96.5	8.8	1012	070304	070304 mus musculu
19	95.5	8.7	1406	09W6V5	09w6v5 gallus gall
20	93.5	8.5	929	09VRJ2	09vrj2 drosophila
21	93.5	8.5	947	07RDK2	07rkd2 plasmodium
22	92.5	8.4	1153	1 NOS_LYMST	061309 lymnaea sca
23	91.5	8.3	823	08CEB4	08ceb4 mus musculu
24	91.5	8.3	1188	1 ITAH_MOUSE	08ceb4 mus musculu
25	91.5	8.3	1188	1 ITAH_MOUSE	08ceb4 mus musculu
26	91.5	8.3	623	1 SYR_SUITO	0971x1 sulfolobus
27	90	8.2	716	08C449	08c449 mus musculu
28	90	8.2	754	08BRK4	08brk4 mus musculu
29	90	8.2	799	1 CAD8_MOUSE	097291 mus musculu
30	90	8.2	799	1 CAD8_MOUSE	054800 ractus norv
31	90	8.2	1608	2 07PR41	07pr41 anopheles g

32	89.5	8.1	161	2 09WUP8	09wup8 ractus norv
33	89.5	8.1	244	2 09CEE1	09cee1 aradidopsis
34	89.5	8.1	1063	1 ITN8_HUMAN	09c6e1 aradidopsis
35	89.5	8.1	1188	2 076326	076326 drosophila
36	89	8.1	481	2 06W465	06w465 paracchlamyd
37	89	8.1	799	1 CAD8_HUMAN	06w465 paracchlamyd
38	89	8.1	1054	2 09U651	09u651 strongyloce
39	88.5	8.0	656	2 09QU36	09qu36 ttv-like m
40	88	8.0	580	2 08OX37	08ox37 mus musculu
41	88	8.0	778	1 CD4_MOUSE	08ox37 mus musculu
42	87	7.9	362	1 CD4_CRIGR	08ox37 mus musculu
43	87	7.9	716	2 09D001	09d001 mus musculu
44	87	7.9	498	2 08C375	08c375 mus musculu
45	87	7.9	1326	2 08GH34	08gh34 paenibacill
46	86.5	7.8	252	2 09FX00	09fx00 aradidopsis
47	86.5	7.8	956	2 09W4T9	09w4t9 drosophila
48	86.5	7.8	1063	2 08KX00	08kx00 chlorobium
49	86	7.8	364	2 070509	070509 ractus norv
50	86	7.8	431	1 CD4_MESAU	060522 m cd44 ant
51	86	7.8	503	1 CD4_RAT	060522 m cd44 ant
52	86	7.8	780	2 008779	008779 ractus norv
53	85.5	7.8	667	2 09M3D7	09m3d7 aradidopsis
54	85.5	7.8	826	2 081Y15	081y15 homo sapien
55	85.5	7.8	959	2 09N9Y9	09n9y9 drosophila
56	85.5	7.8	975	2 097174	097174 drosophila
57	85.5	7.8	1148	2 09H7S7	09h7s7 homo sapien
58	85.5	7.8	1865	2 09HCM3	09hcm3 homo sapien
59	84.5	7.7	252	2 09FGB3	09fgb3 aradidopsis
60	84.5	7.7	468	2 09JVK7	09jvk7 neisseria m
61	84.5	7.7	536	1 FLIF_BACSV	09jvk7 neisseria m
62	84.5	7.7	823	2 08WY18	08wy18 homo sapien
63	84.5	7.7	1033	2 042598	042598 xenopus lae
64	84.5	7.7	1112	2 002344	002344 caenorhabdi
65	84	7.6	261	2 08REU8	08reu8 fusobacteri
66	84	7.6	428	2 09M029	09m029 aradidopsis
67	84	7.6	677	2 08EQW3	08eqw3 oceanobacil
68	83.5	7.6	444	2 06DBH0	06dbh0 aradidopsis
69	83.5	7.6	1337	1 PPRJ_HUMAN	012913 homo sapien
70	83.5	7.6	4464	2 07RL36	07rl36 plasmodium
71	83	7.5	311	2 08PS66	08ps66 methanosaer
72	83	7.5	317	2 097310	097310 plasmodium
73	83	7.5	364	2 098028	098028 diceror bic
74	83	7.5	403	2 096276	096276 sulfolobus
75	83	7.5	525	2 09K432	09k432 bacillus ha
76	83	7.5	1185	2 07PRK4	07prk4 anopheles g
77	82.5	7.5	307	2 06W799	06w799 brachydanto
78	82.5	7.5	330	2 007474	007474 staphylococ
79	82.5	7.5	436	2 09BK19	09bk19 caenorhabdi
80	82.5	7.5	465	2 018591	018591 caenorhabdi
81	82.5	7.5	527	2 0837F6	0837f6 enterococcu
82	82.5	7.5	1044	1 ITN8_CHICK	026009 gallus gall
83	82	7.4	1122	2 06FX04	06fx04 candida gla
84	82	7.4	1189	1 ITAH_HUMAN	09ukx5 homo sapien
85	82	7.4	1216	2 062884	062884 ractus norv
86	81.5	7.4	224	2 08VSW8	08vsw8 staphylococ
87	81.5	7.4	252	2 065701	065701 aradidopsis
88	81.5	7.4	263	1 LEU3_PHOIL	07n128 photorhabdi
89	81.5	7.4	615	2 0740R0	0740r0 mycobacteri
90	81.5	7.4	773	2 08TGH3	08tgh3 malassezia
91	81.5	7.4	800	2 086LP9	086lp9 drosophila
92	81.5	7.4	801	2 086LP8	086lp8 drosophila
93	81.5	7.4	1048	1 ITAV_HUMAN	086v08 homo sapien
94	81	7.4	191	2 089V08	089v08 bradyrhizob
95	81	7.4	1041	2 076378	076378 lyechinus
96	81	7.4	1041	2 09UB90	09ub90 lyechinus
97	81	7.4	1179	1 ITA7_MOUSE	061308 mus musculu
98	80.5	7.3	257	2 08RB06	08rb06 thermoaer
99	80.5	7.3	316	2 09ZML8	09zml8 rhizobium m
100	80.5	7.3	524	2 06FRP5	06frp5 acinetobact
101	80.5	7.3	673	2 095YMO	095ymo polyandroca
102	80.5	7.3	675	2 09F014	09f014 aradidopsis
103	80.5	7.3	803	2 06EV15	06ev15 candida gla
104	80.5	7.3	857	2 090YJ4	090yj4 brachydanto

105	80.5	7.3	1034	1	ITAV CHICK	P26008 gallus galli	178	77	7.0	1263	2	Q7M8C9	Q7M8C9 wolinnella s
106	80.5	7.3	6995	2	Q66RK2	Q66RK2 homo sapien	179	76.5	6.9	203	2	Q7Z552	Q7Z552 homo sapien
107	80.5	7.3	22155	2	Q68K17	Q68K17 homo sapien	180	76.5	6.9	206	2	Q6CP95	Q6CP95 simian adien
108	80	7.3	234	1	VGP8_EBV	P03224 Epstein-Bar	181	76.5	6.9	304	2	Q9BVA9	Q9BVA9 homo sapien
109	80	7.3	234	2	Q777C5	Q777C5 human herpe	182	76.5	6.9	326	2	Q814P0	Q814P0 plasmodium
110	80	7.3	489	2	Q6UAK6	Q6UAK6 agrobacteri	183	76.5	6.9	353	2	Q7TIC1	Q7TIC1 brachydanio
111	80	7.3	1696	2	Q6FXA2	Q6FXA2 candida gla	184	76.5	6.9	357	2	Q73XD7	Q73XD7 treponema d
112	79.5	7.2	175	2	Q80Y67	Q80Y67 mus musculu	185	76.5	6.9	363	1	LEU3_SALTY	P37412 salmonella
113	79.5	7.2	275	1	Q64A68	Q64A68 uncultured	186	76.5	6.9	365	1	QPSR_XENLA	O12948 xenopus lae
114	79.5	7.2	393	1	ITL5_CERAE	Q29612 cercopithec	187	76.5	6.9	385	2	Q8V3D0	Q8V3D0 swinepox vi
115	79.5	7.2	502	2	Q82FJ2	Q82FJ2 streptomyce	188	76.5	6.9	475	1	MUC1_HYLLA	Q29435 hylobates l
116	79.5	7.2	543	2	Q6XN32	Q6XN32 rhodococcos	189	76.5	6.9	549	2	Q9NOS3	Q9NOS3 homo sapien
117	79.5	7.2	616	2	Q9Y1A2	Q9Y1A2 trypanosoma	190	76.5	6.9	568	2	Q870Y7	Q870Y7 neurospora
118	79.5	7.2	1044	1	ITAV MOUSE	P43405 mus musculu	191	76.5	6.9	632	2	Q9P4X1	Q9P4X1 s glycoprot
119	79	7.2	181	2	Q9G0D5	Q9G0D5 eriocheir s	192	76.5	6.9	794	1	Q93264	Q93264 xenopus lae
120	79	7.2	370	2	Q7T5N7	Q7T5N7 mus musculu	193	76.5	6.9	895	2	Q89EH8	Q89EH8 bradyrhizob
121	79	7.2	398	2	Q9JIE1	Q9JIE1 mus musculu	194	76.5	6.9	945	2	Q6L4G5	Q6L4G5 solanum dem
122	79	7.2	437	1	YC44_PORPU	P51363 porphyra pu	195	76	6.9	180	2	Q9Y647	Q9Y647 aetopyrum p
123	79	7.2	550	2	Q8K0G0	Q8K0G0 mus musculu	196	76	6.9	253	2	Q8UZE2	Q8UZE2 cercopithec
124	79	7.2	555	2	Q8BKU8	Q8BKU8 mus musculu	197	76	6.9	291	2	Q86PD7	Q86PD7 schistosoma
125	79	7.2	611	1	RBT3 MOUSE	Q9CTN4 mus musculu	198	76	6.9	306	2	Q98RE9	Q98RE9 mycoplasma
126	79	7.2	718	2	Q65DD6	Q65DD6 bacillus li	199	76	6.9	362	2	Q98029	Q98029 diceros bic
127	79	7.2	916	2	Q68WR4	Q68WR4 rickettsia	200	76	6.9	369	2	Q98PW1	Q98PW1 mycoplasma
128	79	7.2	1016	2	Q91779	Q91779 xenopus lae	201	76	6.9	399	2	Q9ERS5	Q9ERS5 mus musculu
129	79	7.2	1033	1	ITAB MOUSE	Q9GUM0 mus musculu	202	76	6.9	542	2	Q60113	Q60113 schizosacch
130	79	7.2	1597	2	Q36OM3	Q36OM3 drosophila	203	76	6.9	614	2	Q29599	Q29599 archaeglob
131	79	7.2	2029	1	LAR DROME	P16621 drosophila	204	76	6.9	781	2	Q6TOD9	Q6TOD9 caenorhabdi
132	79	7.2	2029	2	Q9VTG8	Q9VTG8 drosophila	205	76	6.9	951	2	Q7WUT4	Q7WUT4 rhodoptere11
133	79	7.2	4057	2	Q81J67	Q81J67 plasmodium	206	76	6.9	1023	2	Q95293	Q95293 leishmania
134	78.5	7.1	422	2	Q82WK0	Q82WK0 nitrosomona	207	76	6.9	1023	2	Q8AY58	Q8AY58 fundulus he
135	78.5	7.1	548	2	Q9ZDV5	Q9ZDV5 rickettsia	208	76	6.9	1036	2	Q9TUV4	Q9TUV4 canis fam11
136	78.5	7.1	633	2	Q7SE53	Q7SE53 neurospora	209	76	6.9	1036	2	Q9TUN8	Q9TUN8 canis fam11
137	78.5	7.1	930	2	Q8IO48	Q8IO48 drosophila	210	76	6.9	1337	1	YDM5_SCHPO	P87136 schizosacch
138	78.5	7.1	970	2	Q9U6L4	Q9U6L4 drosophila	211	76	6.9	1416	2	Q7JMN2	Q7JMN2 anopheles g
139	78.5	7.1	1047	1	ITAV BOVIN	P80746 bos taurus	212	76	6.9	1509	2	Q7JMA7	Q7JMA7 caenorhabdi
140	78.5	7.1	1577	2	Q6BUX5	Q6BUX5 debaryomyce	213	76	6.9	1546	2	Q75D74	Q75D74 aeshya goss
141	78	7.1	290	2	Q8AUN0	Q8AUN0 paratydoc	214	76	6.9	1692	2	Q7JM48	Q7JM48 caenorhabdi
142	78	7.1	290	2	Q8AUZ6	Q8AUZ6 aetacotillap	215	76	6.9	1888	2	Q7JM45	Q7JM45 caenorhabdi
143	78	7.1	290	2	Q8AUZ8	Q8AUZ8 gaurochromi	216	76	6.9	1927	2	Q7JM46	Q7JM46 caenorhabdi
144	78	7.1	343	1	MRGF RAT	P23749 rattus norv	217	76	6.9	2048	2	Q7JMA2	Q7JMA2 caenorhabdi
145	78	7.1	377	2	Q341E1	Q341E1 salmonella	218	76	6.9	2066	2	Q22190	Q22190 caenorhabdi
146	78	7.1	377	2	Q7CQ01	Q7CQ01 salmonella	219	76	6.9	2101	2	Q7JMA3	Q7JMA3 caenorhabdi
147	78	7.1	504	2	O13102	O13102 carassius a	220	76	6.9	2134	2	Q7JM44	Q7JM44 caenorhabdi
148	78	7.1	519	2	Q90425	Q90425 brachydanio	221	76	6.9	2344	2	Q86119	Q86119 rabbit hemo
149	78	7.1	555	2	Q96K49	Q96K49 homo sapien	222	75.5	6.9	125	2	Q7MBJ0	Q7MBJ0 vibrlo valn
150	78	7.1	732	1	CADL_CHICK	P33145 gallus galli	223	75.5	6.9	230	2	Q8YRJ3	Q8YRJ3 anabaena sp
151	78	7.1	1022	1	A1A1_ANGAN	Q97030 anguilla an	224	75.5	6.9	264	2	Q649N8	Q649N8 uncultured
152	78	7.1	1171	2	Q42054	Q42054 gallus galli	225	75.5	6.9	282	2	Q7PYU2	Q7PYU2 anopheles g
153	78	7.1	2344	2	Q86117	Q86117 rabbit hemo	226	75.5	6.9	335	2	Q15055	Q15055 homo sapien
154	77.5	7.0	263	2	Q7P3V5	Q7P3V5 fusobacteri	227	75.5	6.9	348	2	Q7VNT3	Q7VNT3 haemophilus
155	77.5	7.0	307	2	Q74P63	Q74P63 bacillus ce	228	75.5	6.9	350	2	Q7YMU5	Q7YMU5 porphyromon
156	77.5	7.0	340	2	Q8GAT5	Q8GAT5 primary end	229	75.5	6.9	357	2	Q7YPO6	Q7YPO6 oncorhynch
157	77.5	7.0	351	1	CD44_CANFA	Q28284 canis fam11	230	75.5	6.9	370	2	Q811Z9	Q811Z9 plasmodium
158	77.5	7.0	468	2	Q9XOK1	Q9XOK1 neisseria m	231	75.5	6.9	385	2	Q6FDV1	Q6FDV1 actinobact
159	77.5	7.0	532	2	Q8KIT2	Q8KIT2 primary end	232	75.5	6.9	407	2	Q9Y412	Q9Y412 homo sapien
160	77.5	7.0	686	2	Q9RDS3	Q9RDS3 streptomyce	233	75.5	6.9	425	2	Q8A990	Q8A990 bacteroides
161	77.5	7.0	751	2	Q8ILK0	Q8ILK0 plasmodium	234	75.5	6.9	507	2	Q8B117	Q8B117 parana viru
162	77.5	7.0	817	2	Q6ZPN1	Q6ZPN1 mus musculu	235	75.5	6.9	507	2	Q8B120	Q8B120 parana viru
163	77.5	7.0	991	2	Q7Z119	Q7Z119 alypsia cal	236	75.5	6.9	549	1	YXCE_ECOLI1	P373703 escherichia
164	77.5	7.0	1499	2	Q990815	Q990815 gallus galli	237	75.5	6.9	619	2	Q8SXH6	Q8SXH6 drosophila
165	77.5	7.0	1727	2	Q68FD9	Q68FD9 mus musculu	238	75.5	6.9	653	2	O02329	O02329 caenorhabdi
166	77	7.0	308	2	Q83NU6	Q83NU6 tiropheyria	239	75.5	6.9	1255	1	MUC1_HUMAN	P15941 h mucin 1 p
167	77	7.0	318	2	Q66S57	Q66S57 oikopleura	240	75.5	6.9	1335	2	Q9GP66	Q9GP66 drosophila
168	77	7.0	322	1	GPT_SULISO	P96000 sulfolobus	241	75.5	6.9	1713	2	Q9W155	Q9W155 drosophila
169	77	7.0	357	2	Q6J5K1	Q6J5K1 tetradom n	242	75.5	6.9	1713	2	Q7KM98	Q7KM98 drosophila
170	77	7.0	357	2	Q6J5K2	Q6J5K2 fugu rubrip	243	75	6.8	272	2	Q889A5	Q889A5 pseudomonas
171	77	7.0	366	2	Q27515	Q27515 methanobact	244	75	6.8	290	2	Q8AUZ7	Q8AUZ7 aetacotillap
172	77	7.0	388	2	Q8G583	Q8G583 methanobact	245	75	6.8	290	2	Q8AUZ7	Q8AUZ7 gaurochromi
173	77	7.0	435	2	Q8E963	Q8E963 shewanella	246	75	6.8	321	2	Q6INFO	Q6INFO xenopus lae
174	77	7.0	459	2	Q8G3W8	Q8G3W8 bifidobacte	247	75	6.8	331	1	MRGF MOUSE	Q8VCJ6 mus musculu
175	77	7.0	541	2	Q97DN5	Q97DN5 clostridium	248	75	6.8	357	1	QPSR_ORYLA	P87357 oryzias lat
176	77	7.0	699	2	Q6YVW8	Q6YVW8 oryza gativ	249	75	6.8	538	2	Q87359	Q87359 staphylococ
177	77	7.0	1045	2	Q91292	Q91292 pleurodeles	250	75	6.8	538	2	Q7WU24	Q7WU24 staphylococ

251	75	6.8	668	2	07F0M5	07f0m5	Oryza sativ	324	73.5	6.7	301	2	08BYV9	08BYV9	mycoplasma
252	75	6.8	909	2	06FOBO	06foBO	caenorhabdi	325	73.5	6.7	307	2	0645Y3	0645Y3	gorilla gor
253	75	6.8	997	2	06GJ02	06gJ02	xenopus lae	326	73.5	6.7	321	2	0817D0	0817D0	liseria mo
254	75	6.8	1007	1	GRD2_MOUSE	GRD2_MOUSE	mus musculu	327	73.5	6.7	349	2	08HX41	08HX41	saimo salar
255	75	6.8	1007	1	GRD2_MOUSE	GRD2_MOUSE	mus musculu	328	73.5	6.7	328	2	06ZHF3	06ZHF3	burkholderi
256	75	6.8	1037	2	06E1Y7	06e1Y7	brachydanio	329	73.5	6.7	465	1	FTH1_YEAST	FTH1_YEAST	saccharomyc
257	75	6.8	1216	2	090Y55	090Y55	brachydanio	330	73.5	6.7	485	2	010430	010430	junin arena
258	75	6.8	1254	2	090Y56	090Y56	brachydanio	331	73.5	6.7	485	2	0642U8	0642U8	junin arena
259	75	6.8	1254	2	09YH02	09YH02	brachydanio	332	73.5	6.7	488	2	06GPA2	06GPA2	caenorhabdi
260	75	6.8	1428	1	ATRN_MOUSE	ATRN_MOUSE	mus musculu	333	73.5	6.7	553	2	09MZ11	09MZ11	macaca mula
261	74.5	6.8	204	2	08UY72	08uy72	simian aden	334	73.5	6.7	563	2	08FBU5	08FBU5	corynebacte
262	74.5	6.8	207	2	064YV0	064YV0	bacteroides	335	73.5	6.7	578	2	083EB6	083EB6	coxiella bu
263	74.5	6.8	230	2	06FOV9	06foV9	mesoplasma	336	73.5	6.7	624	2	09SHN0	09SHN0	arabidopsis
264	74.5	6.8	257	2	08BAP8	08BAP8	thermonaer	337	73.5	6.7	636	1	MUCL_MOUSE	MUCL_MOUSE	mus musculu
265	74.5	6.8	259	2	08NAX8	08nax8	aedes trise	338	73.5	6.7	630	2	022040	022040	caenorhabdi
266	74.5	6.8	307	1	TR41_HUMAN	TR41_HUMAN	homo sapien	339	73.5	6.7	656	2	08TWM1	08TWM1	methanopyru
267	74.5	6.8	348	1	RNPD_VIBPA	08Tmx1	vibrio para	340	73.5	6.7	782	2	037353	037353	lymantria d
268	74.5	6.8	379	1	MCP_CAVPO	P70105	cavia porce	341	73.5	6.7	783	2	09YMR1	09YMR1	lymantria d
269	74.5	6.8	469	2	09NC94	09nc94	trypanosoma	342	73.5	6.7	785	1	CAD7_HUMAN	CAD7_HUMAN	homo sapien
270	74.5	6.8	522	2	09YPA0	09YPA0	canine hept	343	73.5	6.7	796	1	CAD8_MOUSE	CAD8_MOUSE	mus musculu
271	74.5	6.8	549	2	07A924	07a924	escherichia	344	73.5	6.7	796	2	08C7Q6	08C7Q6	mus musculu
272	74.5	6.8	549	2	08X5U0	08x5U0	escherichia	345	73.5	6.7	857	2	06B3P0	06B3P0	brachydanio
273	74.5	6.8	549	2	08EPAZ5	08EPAZ5	escherichia	346	73.5	6.7	1025	2	09DBU1	09DBU1	brachydanio
274	74.5	6.8	549	2	083IR1	083IR1	shigella fl	347	73.5	6.7	1056	2	08BPJ1	08BPJ1	xanthomonas
275	74.5	6.8	631	2	099K60	099K60	mus musculu	348	73.5	6.7	1166	2	096219	096219	plasmodium
276	74.5	6.8	664	2	09M3D8	09m3D8	arabidopsis	349	73.5	6.7	1179	2	07Z017	07Z017	aedes aegypt
277	74.5	6.8	719	2	06YX22	06YX22	Oryza sativ	350	73.5	6.7	1179	2	09MCO0	09MCO0	mus musculu
278	74.5	6.8	750	2	06YX21	06YX21	Oryza sativ	351	73.5	6.7	1188	2	08E0Y1	08E0Y1	shewanella
279	74.5	6.8	787	2	07OHQ3	07OHQ3	anopheles g	352	73.5	6.7	1213	1	JAG3_BRARE	JAG3_BRARE	brachydanio
280	74.5	6.8	906	2	09XPY4	09XPY4	trypanosoma	353	73.5	6.7	1721	2	061450	061450	solanum dem
281	74.5	6.8	2244	2	0980F2	0980F2	trypanosoma	354	73.5	6.7	1889	2	0700X2	0700X2	anopheles g
282	74	6.7	199	2	06OPG7	06OPG7	simian aden	355	73.5	6.7	2573	2	061432	061432	solanum dem
283	74	6.7	281	2	08SCJ1	08scJ1	mus musculu	356	73.5	6.7	3350	2	08YVE1	08YVE1	tanana bat
284	74	6.7	288	2	06HDM4	06hdm4	bacillus th	357	73.5	6.7	5054	2	07REU1	07REU1	plasmodium
285	74	6.7	290	2	08A0U1	08A0U1	labeotrophe	358	73	6.6	264	2	07Q5X1	07Q5X1	anopheles g
286	74	6.7	290	2	08A0U3	08A0U3	tyranochro	359	73	6.6	290	2	08A0Z3	08A0Z3	autonocara
287	74	6.7	290	2	08A0U3	08A0U3	pseudotroph	360	73	6.6	290	2	08A0Z9	08A0Z9	gaurochroa
288	74	6.7	290	2	08A0U4	08A0U4	protomelas	361	73	6.6	290	2	08A0V1	08A0V1	paralabidoc
289	74	6.7	290	2	08A0U2	08A0U2	taenioletr	362	73	6.6	290	2	08A0V2	08A0V2	paralabidoc
290	74	6.7	290	2	08A0U3	08A0U3	melanochrom	363	73	6.6	302	2	09MW83	09MW83	lactococcus
291	74	6.7	290	2	08A0U4	08A0U4	autonocara	364	73	6.6	304	2	08U937	08U937	agrobacteri
292	74	6.7	290	2	08A0U0	08A0U0	melanochrom	365	73	6.6	315	2	09ZC71	09ZC71	yerfina pe
293	74	6.7	290	2	08A0U1	08A0U1	cytiocillapla	366	73	6.6	326	2	07X9Q7	07X9Q7	cucumis mel
294	74	6.7	290	2	08A0U0	08A0U0	tyranochro	367	73	6.6	343	2	08A1U5	08A1U5	bacillus an
295	74	6.7	290	2	08A0U1	08A0U1	pseudotroph	368	73	6.6	357	2	07R2U3	07R2U3	bacillus ce
296	74	6.7	290	2	08A0U2	08A0U2	cytiocillapla	369	73	6.6	357	2	091915	091915	oreochromis
297	74	6.7	290	2	08A0U4	08A0U4	autonocara	370	73	6.6	371	2	09SE64	09SE64	dumasia vil
298	74	6.7	311	1	08LMY4	08LMY4	lamnaria d	371	73	6.6	374	2	061377	061377	bacillus an
299	74	6.7	357	2	08LMY4	08LMY4	carassius a	372	73	6.6	374	2	063FT6	063FT6	bacillus ce
300	74	6.7	357	2	08LMY4	08LMY4	carassius a	373	73	6.6	374	2	073DD3	073DD3	bacillus th
301	74	6.7	357	2	068YX7	068YX7	haplochromi	374	73	6.6	374	2	06HNA5	06HNA5	canis famil
302	74	6.7	357	2	078C19	078C19	metriacelma	375	73	6.6	381	2	030428	030428	bacillus ce
303	74	6.7	357	2	091853	091853	dimidiocro	376	73	6.6	415	2	0813R3	0813R3	mycoplasma
304	74	6.7	357	2	091857	091857	labeotrophe	377	73	6.6	512	1	SYM_MYCGE	SYM_MYCGE	carcinus ma
305	74	6.7	371	2	073JG1	073JG1	treponema d	378	73	6.6	673	2	0237Q6	0237Q6	bacteroides
306	74	6.7	494	2	08DWM1	08dwm1	streptococc	379	73	6.6	777	2	08A9P3	08A9P3	xenopus lae
307	74	6.7	510	2	07A1D6	07A1D6	lactobacilli	380	73	6.6	780	2	006271	006271	caenorhabdi
308	74	6.7	546	2	0610W9	0610W9	picropilius	381	73	6.6	1006	2	096608	096608	caenorhabdi
309	74	6.7	589	2	09R9H8	09r9H8	bacillus su	382	73	6.6	1181	1	ITR2_HUMAN	ITR2_HUMAN	homo sapien
310	74	6.7	589	2	09R9H8	09R9H8	bacillus su	383	73	6.6	1244	2	06FNZ1	06FNZ1	candida gla
311	74	6.7	626	2	090880	090880	gallus gall	384	73	6.6	1250	2	086RA5	086RA5	drosophila
312	74	6.7	626	2	098922	098922	gallus gall	385	73	6.6	2344	2	089273	089273	rabbit hemo
313	74	6.7	681	2	06ZFS6	06zfs6	Oryza sativ	386	73	6.6	5010	2	081CV2	081CV2	mus musculu
314	74	6.7	925	2	07YYU8	07YYU8	cryptospori	387	72.5	6.6	144	2	06QGY4	06QGY4	citrellus l
315	74	6.7	1056	2	08P875	08P875	xanthomonas	388	72.5	6.6	185	2	06AGU7	06AGU7	leishmania x
316	74	6.7	1059	2	08CHFO	08chfo	mus musculu	389	72.5	6.6	193	2	060551	060551	mesocricetu
317	74	6.7	1115	2	0751K4	0751K4	asbhyia goes	390	72.5	6.6	291	2	08C1X2	08C1X2	mus musculu
318	73.5	6.7	94	1	FXV6_MOUSE	09A164	mus musculu	391	72.5	6.6	299	1	CD80_RABIT	CD80_RABIT	cyrcolagus
319	73.5	6.7	94	1	FXV6_MOUSE	09A164	mus musculu	392	72.5	6.6	426	2	P796D7	P796D7	phoca vitul
320	73.5	6.7	154	2	09Y4K8	09Y4K8	drosophila	393	72.5	6.6	426	2	09C1H8	09C1H8	pasteurella
321	73.5	6.7	229	2	07Z546	07Z546	homo sapien	394	72.5	6.6	440	1	HEM1_HELHP	HEM1_HELHP	helicobacte
322	73.5	6.7	278	2	087IR5	087IR5	vibrio para	395	72.5	6.6	541	2	09DSJO	09DSJO	human immun
323	73.5	6.7	280	2	09A149	09A149	burkholderi	396	72.5	6.6	682	2	09M3B5	09M3B5	arabidopsis

397	72.5	6.6	905	2	Q7N649	Q7N649 photorhabdu	470	71	6.4	98	2	Q8E2T7	Q8E2T7 streptococc
398	72.5	6.6	913	2	Q86AX0	Q86AX0 brachyocelli	471	71	6.4	118	2	Q83GY2	Q83GY2 tropheryma
399	72.5	6.6	1035	2	Q6OAR3	Q6OAR3 bacchydanio	472	71	6.4	157	2	Q66WB3	Q66WB3 hesperia co
400	72.5	6.6	1050	1	ITR5_XENIA	Q6E274 xenopus lae	473	71	6.4	157	2	Q66WB6	Q66WB6 hesperia co
401	72.5	6.6	1222	2	Q8MYT6	Q8MYT6 sexostrea e	474	71	6.4	157	2	Q66WC9	Q66WC9 hesperia co
402	72.5	6.6	2873	1	RBP1_PLAVB	Q00798 plasmodium	475	71	6.4	183	2	Q96WQ8	Q96WQ8 homo sapien
403	72	6.5	93	2	Q641S5	Q641S5 xenopus lae	476	71	6.4	225	2	Q9TQJ9	Q9TQJ9 proteus vul
404	72	6.5	290	2	Q8AU9	Q8AU9 neochromis	477	71	6.4	225	2	Q81270	Q81270 proteus vul
405	72	6.5	290	2	Q8AU9	Q8AU9 haplochromi	478	71	6.4	235	2	Q8WYN2	Q8WYN2 homo sapien
406	72	6.5	290	2	Q8AU9	Q8AU9 haplochromi	479	71	6.4	250	2	Q72ED8	Q72ED8 desulfovibr
407	72	6.5	290	2	Q8AUP9	Q8AUP9 haplochromi	480	71	6.4	262	2	Q23480	Q23480 caenorhadi
408	72	6.5	290	2	Q8AUP9	Q8AUP9 astacoreoch	481	71	6.4	274	2	Q92LM1	Q92LM1 rnziodium m
409	72	6.5	290	2	Q8AUP9	Q8AUP9 haplochromi	482	71	6.4	290	2	Q8AUV3	Q8AUV3 ysaichromis
410	72	6.5	290	2	Q8AUV3	Q8AUV3 parablodoc	483	71	6.4	292	2	Q8WNV1	Q8WNV1 bos taurus
411	72	6.5	302	2	Q6ASU7	Q6ASU7 ysaichromis	484	71	6.4	316	2	Q9F3S9	Q9F3S9 rhodothermu
412	72	6.5	361	2	Q86T72	Q86T72 bacteroides	485	71	6.4	321	2	Q92C01	Q92C01 listeria in
413	72	6.5	374	2	Q93N69	Q93N69 homo sapien	486	71	6.4	303	2	Q7ZXR4	Q7ZXR4 xenopus lae
414	72	6.5	379	2	Q7Q0J1	Q7Q0J1 anopheles ce	487	71	6.4	305	2	Q8EQS0	Q8EQS0 oceanobacil
415	72	6.5	439	2	Q8ZPD1	Q8ZPD1 salmonella	488	71	6.4	306	2	Q81M30	Q81M30 bacillus an
416	72	6.5	479	2	Q8M9Q3	Q8M9Q3 globularia	489	71	6.4	307	2	Q7R3F7	Q7R3F7 giardia lam
417	72	6.5	485	2	Q8ZSH2	Q8ZSH2 anabaena sp	490	71	6.4	316	2	Q9F3S9	Q9F3S9 rhodothermu
418	72	6.5	486	2	Q8GYU4	Q8GYU4 seipia offic	491	71	6.4	321	2	Q92C01	Q92C01 listeria in
419	72	6.5	518	2	Q6C3U1	Q6C3U1 yarrowia li	492	71	6.4	325	2	Q924S3	Q924S3 rictus norv
420	72	6.5	526	2	Q74292	Q74292 gibberella	493	71	6.4	326	1	TEL2_YEAST	TEL2_YEAST
421	72	6.5	543	2	Q16749	Q16749 caenorhadi	494	71	6.4	326	1	Q6Q5U9	Q6Q5U9 saccharomyc
422	72	6.5	588	2	Q9VGA8	Q9VGA8 drosophila	495	71	6.4	327	2	Q9GEZ3	Q9GEZ3 gymnosteris
423	72	6.5	591	2	Q6BKJ7	Q6BKJ7 debaryomyce	496	71	6.4	335	2	Q8N9J3	Q8N9J3 homo sapien
424	72	6.5	674	2	Q84EP8	Q84EP8 pseudomonas	497	71	6.4	335	2	Q9GEZ1	Q9GEZ1 ipomopsis a
425	72	6.5	760	2	Q9FC45	Q9FC45 streptomyce	498	71	6.4	336	2	Q8JH12	Q8JH12 brachydario
426	72	6.5	787	2	Q616S1	Q616S1 oryza sativ	499	71	6.4	338	2	Q9H5A4	Q9H5A4 homo sapien
427	72	6.5	792	1	CADB_CH1CK	Q9J319 gallus gall	500	71	6.4	342	2	Q8G2J3	Q8G2J3 bruceia su
428	72	6.5	865	2	Q7EZ33	Q7EZ33 oryza sativ	501	71	6.4	342	2	Q7ZXJ4	Q7ZXJ4 xenopus lae
429	72	6.5	877	2	Q8S6D6	Q8S6D6 oryza sativ	502	71	6.4	347	2	Q6S8M7	Q6S8M7 homo sapien
430	72	6.5	1007	1	GRD2_HUMAN	Q43424 homo sapien	503	71	6.4	358	2	Q81HG8	Q81HG8 drosophila
431	72	6.5	1036	1	V414_MYCSE	P47653 mycoplasma	504	71	6.4	358	1	Q8MLK6	Q8MLK6 drosophila
432	72	6.5	1106	1	ITAT_RAT	Q63258 rattus norv	505	71	6.4	366	1	CD44_BOVIN	CD44_BOVIN
433	72	6.5	1293	2	Q9UIQ9	Q9UIQ9 caenorhadi	506	71	6.4	366	1	YN10_YEAST	YN10_YEAST
434	72	6.5	1436	2	Q96ZJ5	Q96ZJ5 bulfolobus	507	71	6.4	423	2	Q8A1Z3	Q8A1Z3 bacteroides
435	72	6.5	1795	2	Q6MUJ8	Q6MUJ8 mycoplasma	508	71	6.4	463	2	Q8X1Y7	Q8X1Y7 clostridium
436	72	6.5	2344	2	Q9EMC2	Q9EMC2 rabbit hemo	509	71	6.4	463	2	Q68AX5	Q68AX5 fugu rubrip
437	72	6.5	3251	2	Q8K4E0	Q8K4E0 mus musculu	510	71	6.4	463	2	Q68AX6	Q68AX6 fugu rubrip
438	72	6.5	5005	2	Q9PZP5	Q9PZP5 ureaplasma	511	71	6.4	470	2	Q9H5A6	Q9H5A6 homo sapien
439	72	6.5	97	2	Q6S7D6	Q6S7D6 sus scrofa	512	71	6.4	482	2	Q7O1B7	Q7O1B7 calceolaria
440	71.5	6.5	207	2	Q6LYX0	Q6LYX0 mechanococc	513	71	6.4	489	2	Q8Y6R6	Q8Y6R6 listeria mo
441	71.5	6.5	258	2	Q67JMO	Q67JMO symbiobacte	514	71	6.4	489	2	Q92B92	Q92B92 listeria in
442	71.5	6.5	268	2	Q7Z547	Q7Z547 homo sapien	515	71	6.4	493	2	Q86Z27	Q86Z27 homo sapien
443	71.5	6.5	331	1	ISPH_LISMO	P56676 listeria mo	516	71	6.4	499	2	Q8BY50	Q8BY50 mus musculu
444	71.5	6.5	338	2	Q9S509	Q9S509 leopardus p	517	71	6.4	507	2	Q6A1S2	Q6A1S2 mus musculu
445	71.5	6.5	338	2	Q9S512	Q9S512 leopardus p	518	71	6.4	508	2	Q8FDJ6	Q8FDJ6 echerichia
446	71.5	6.5	364	2	Q8HX60	Q8HX60 sus scrofa	519	71	6.4	513	2	Q9NKV9	Q9NKV9 drosophila
447	71.5	6.5	375	2	Q6S280	Q6S280 african swi	520	71	6.4	514	2	Q629J3	Q629J3 rattus norv
448	71.5	6.5	453	2	Q84414	Q84414 chlamydia t	521	71	6.4	533	2	Q9YCP8	Q9YCP8 aeropyrum p
449	71.5	6.5	506	2	Q7YXQ9	Q7YXQ9 avicennia g	522	71	6.4	548	2	Q6AXO6	Q6AXO6 rattus norv
450	71.5	6.5	512	2	Q6FXR6	Q6FXR6 candida gla	523	71	6.4	560	1	NWB_HUMAN	NWB_HUMAN
451	71.5	6.5	549	2	Q9JLB9	Q9JLB9 mus musculu	524	71	6.4	572	2	Q8N1A1	Q8N1A1 homo sapien
452	71.5	6.5	620	2	Q74HL2	Q74HL2 lactobacill	525	71	6.4	742	1	CD44_HUMAN	CD44_HUMAN
453	71.5	6.5	640	2	Q81L83	Q81L83 oryza sativ	526	71	6.4	826	2	Q9J7J6	Q9J7J6 homo sapien
454	71.5	6.5	676	1	MUC1_MESAU	Q6Q528 mesocricetu	527	71	6.4	836	2	Q9H5A7	Q9H5A7 clostridium
455	71.5	6.5	692	1	Q9SBT5	Q9SBT5 mesocricetu	528	71	6.4	885	1	ARKB_CLOAB	ARKB_CLOAB
456	71.5	6.5	713	2	Q9VRE0	Q9VRE0 arabidopsis	529	71	6.4	717	2	Q81AF9	Q81AF9 plasmodium
457	71.5	6.5	718	2	Q93ZRS	Q93ZRS arabidopsis	530	71	6.4	719	2	Q9H5A5	Q9H5A5 homo sapien
458	71.5	6.5	718	2	Q9LSR8	Q9LSR8 arabidopsis	531	71	6.4	742	1	CD44_HUMAN	CD44_HUMAN
459	71.5	6.5	785	2	Q67G09	Q67G09 mus musculu	532	71	6.4	826	2	Q9J7J6	Q9J7J6 homo sapien
460	71.5	6.5	785	2	Q8BM92	Q8BM92 mus musculu	533	71	6.4	836	2	Q6DCD5	Q6DCD5 xenopus lae
461	71.5	6.5	796	1	CADB_HUMAN	P55287 homo sapien	534	71	6.4	894	2	Q7PMF1	Q7PMF1 anopheles g
462	71.5	6.5	796	1	Q96CZ9	Q96CZ9 homo sapien	535	71	6.4	1009	2	Q98S13	Q98S13 electrophor
463	71.5	6.5	837	2	Q6BFW3	Q6BFW3 paramacium	536	71	6.4	1037	2	Q7M075	Q7M075 rattus norv
464	71.5	6.5	837	2	Q81066	Q81066 arabidopsis	537	71	6.4	1097	1	PPDJ_MOUSE	PPDJ_MOUSE
465	71.5	6.5	879	2	Q25141	Q25141 helicobacte	538	71	6.4	1238	1	Q8K3Q2	Q8K3Q2 mus musculu
466	71.5	6.5	936	2	Q8YSNO	Q8YSNO anabaena sp	539	71	6.4	1238	2	Q8CTW9	Q8CTW9 mus musculu
467	71.5	6.5	1038	1	INAI_CAEEL	Q03600 caenorhadi	540	71	6.4	1238	2	Q8CTW9	Q8CTW9 mus musculu
468	71.5	6.5	1139	2	Q84QR0	Q84QR0 oryza sativ	541	71	6.4	1278	2	Q7RMJ9	Q7RMJ9 plasmodium
469	71.5	6.5	1330	2	Q84QR0	Q84QR0 oryza sativ	542	71	6.4	1278	2	Q7RMJ9	Q7RMJ9 plasmodium

543	71	6.4	1415	2	08MJ16	08mj16	boe taurus	616	70	6.4	331	2	Q7V5T6	Q7v5t6	prochloroco
544	71	6.4	1427	2	08VIB7	08vib7	mesocricetu	617	70	6.4	333	2	Q44603	Q44603	caenorthabi
545	71	6.4	1429	1	ATRN_HUMAN	075882	homo sapien	618	70	6.4	335	2	Q7W774	Q7w774	rhipicephal
546	71	6.4	1432	2	09J086	09j086	rattus norv	619	70	6.4	341	2	Q99XH9	Q99xh9	streplococ
547	71	6.4	1501	2	Q7T117	Q7t117	mus musculi	620	70	6.4	342	2	Q8L128	Q8l128	methanosarc
548	71	6.4	1501	2	Q9QW00	Q9qW00	rattus sp.	621	70	6.4	346	2	Q8HK31	Q8hk31	xiphorhynch
549	71	6.4	1502	2	Q9UM81	Q9um81	homo sapien	622	70	6.4	346	2	Q8HK52	Q8hk52	xiphorhynch
550	71	6.4	1863	2	Q64605	Q64605	rattus norv	623	70	6.4	354	2	Q65U34	Q65u34	mannheimia
551	71	6.4	1904	2	Q64699	Q64699	mus musculi	624	70	6.4	362	1	VE61_MRDV	P22119	maize rough
552	71	6.4	1948	1	PINS_HUMAN	Q13332	homo sapien	625	70	6.4	386	2	Q6HLX8	Q6hlx8	homo sapien
553	71	6.4	2344	1	POLN_RHDV	P27410	r non-struct	626	70	6.4	396	2	Q6ZM42	Q6zm42	homo sapien
554	71	6.4	2699	2	Q7RLQ0	Q7rlq0	plasmodium	627	70	6.4	402	2	Q89501	Q89501	african swi
555	71	6.4	3699	2	Q9HFE8	Q9hfe8	schizosacch	628	70	6.4	428	2	Q8L124	Q8l124	chlamydomp
556	71	6.4	5138	2	Q9ZW94	Q9zw94	arabidopsis	629	70	6.4	470	2	Q65J05	Q65j05	baillius li
557	70.5	6.4	154	1	DMS4_PACDA	Q93454	archidopsis	630	70	6.4	488	2	Q7JG56	Q7jg56	wolbachia p
558	70.5	6.4	154	2	Q860J2	Q860j2	glatifla cam	631	70	6.4	489	1	PT94_YEAST	P07390	saccharomyc
559	70.5	6.4	157	2	Q7XV56	Q7xv56	oryza sativ	632	70	6.4	492	2	Q26580	Q26580	schistosoma
560	70.5	6.4	199	2	Q8CB85	Q8cb85	m mus muscu	633	70	6.4	544	2	Q9CF49	Q9cf49	lactococcus
561	70.5	6.4	224	2	Q8CB85	Q8cb85	m mus muscu	634	70	6.4	556	2	Q7VHM0	Q7vhm0	halicobacte
562	70.5	6.4	246	2	Q81P02	Q81p02	baillius an	635	70	6.4	560	2	Q7QW34	Q7qw34	giardia lam
563	70.5	6.4	269	2	Q94F24	Q94f24	arabidopsis	636	70	6.4	644	2	Q6MTU2	Q6mtu2	aspergillus
564	70.5	6.4	291	2	Q8K1AS	Q8k1as	m dretid7/3	637	70	6.4	683	2	Q9VBV7	Q9vbv7	drosophila
565	70.5	6.4	302	2	Q8KJ99	Q8kj99	lactobacill	638	70	6.4	683	2	Q6ZFF5	Q6zff5	oryza sativ
566	70.5	6.4	305	2	Q6HX74	Q6hx74	baillius an	639	70	6.4	701	2	Q7PS25	Q7ps25	anopheles g
567	70.5	6.4	307	2	Q646B2	Q646b2	pan troglod	640	70	6.4	745	2	Q8WST7	Q8wst7	halocynthia
568	70.5	6.4	310	2	Q8BE18	Q8be18	vaccinia vi	641	70	6.4	753	2	Q845W1	Q845w1	burkholderi
569	70.5	6.4	332	2	Q7U8V4	Q7u8v4	synecchoc	642	70	6.4	780	2	Q7K0S5	Q7k0s5	drosophila
570	70.5	6.4	370	2	Q6HH96	Q6hh96	baillius th	643	70	6.4	801	2	Q920M3	Q920m3	mus musculi
571	70.5	6.4	373	2	Q8J5N9	Q8j5n9	african swi	644	70	6.4	813	2	Q64C97	Q64c97	uncultured
572	70.5	6.4	373	2	Q6JHJ1	Q6jhj1	african swi	645	70	6.4	831	2	Q755V1	Q755v1	ashbya goe
573	70.5	6.4	374	2	Q8BDL9	Q8bdl9	pseudomonas	646	70	6.4	921	2	Q8Q533	Q8q533	ponginge her
574	70.5	6.4	422	2	Q9HKX6	Q9hkx6	thermoplas	647	70	6.4	1023	2	Q7ZVY1	Q7zvyl	anas platyr
575	70.5	6.4	431	1	TOLB_WIGBR	Q82262	wiggleswort	648	70	6.4	1039	1	ITAB_HUMAN	P05514	homo sapien
576	70.5	6.4	438	2	Q8E8M9	Q8e8m9	shewanella	649	70	6.4	1073	2	Q7Q6Q8	Q7q6q8	drosophila
577	70.5	6.4	467	2	Q8H199	Q8h199	arabidopsis	650	70	6.4	1078	2	Q7SHS0	Q7shs0	neurospora
578	70.5	6.4	478	2	Q7O1C0	Q7o1c0	calceolaria	651	70	6.4	1178	1	ITR2_MOUSE	Q62469	mus musculi
579	70.5	6.4	516	2	Q48924	Q48924	glycine max	652	70	6.4	1178	2	Q6P1C7	Q6p1c7	mus musculi
580	70.5	6.4	552	2	Q756T8	Q756t8	ashbya goe	653	70	6.4	1212	2	Q43347	Q43347	gallus gall
581	70.5	6.4	561	2	Q9CKX7	Q9ckx7	pasteurella	654	70	6.4	1226	2	Q9V4U3	Q9v4u3	drosophila
582	70.5	6.4	582	2	Q8WPH4	Q8wph4	drosophila	655	70	6.4	1264	2	Q9V4U4	Q9v4u4	drosophila
583	70.5	6.4	584	2	Q22629	Q22629	caenorthabi	656	70	6.4	1357	2	Q7SF20	Q7sf20	neurospora
584	70.5	6.4	617	2	Q952X6	Q952x6	caenorthabi	657	70	6.4	1635	2	Q17368	Q17368	caenorthabi
585	70.5	6.4	736	2	Q6Z1O8	Q6z1o8	oryza sativ	658	70	6.4	1636	1	YN37_YEAST	P48563	saccharomyc
586	70.5	6.4	783	2	Q7R5Y0	Q7r5y0	giardia lam	659	70	6.4	1721	2	Q93547	Q93547	caenorthabi
587	70.5	6.4	783	2	Q6ELI3	Q6eli3	giardia lam	660	70	6.4	2168	1	POLG_PEVU9	Q41174	p genome po
588	70.5	6.4	801	1	CADK_HUMAN	Q9bdc6	homo sapien	661	70	6.4	2168	2	Q8QUZ8	Q8quz8	porcine ent
589	70.5	6.4	837	2	Q86G85	Q86g85	pseudoplusi	662	70	6.4	20925	2	Q8NUX1	Q8njx1	trichoderma
590	70.5	6.4	900	2	Q65474	Q65474	arabidopsis	663	70	6.4	2108	2	Q6S7D8	Q6s7d8	homo scrofa
591	70.5	6.4	999	2	Q8WOP4	Q8wop4	drosophila	664	70	6.3	215	2	Q6ZSK9	Q6zsk9	homo sapien
592	70.5	6.4	1027	1	ALAI_CATCO	Q66g45	oryza sativ	665	70	6.3	222	2	Q917D5	Q917d5	drosophila
593	70.5	6.4	1049	2	Q66QAS	Q66qas	caenorthabi	666	70	6.3	237	2	Q8BCB6	Q8bcb6	trionyx bin
594	70.5	6.4	1121	2	Q61931	Q61931	caenorthabi	667	70	6.3	244	2	Q720M5	Q720m5	listeria mo
595	70.5	6.4	1166	2	Q7R1F6	Q7r1f6	plasmodium	668	70	6.3	246	2	Q8BTG9	Q8btg9	mus musculi
596	70.5	6.4	1167	2	Q88341	Q88341	rattus norv	669	70	6.3	262	2	Q8RTW4	Q8rtw4	uncultured
597	70.5	6.4	1171	2	Q9V7W8	Q9v7w8	drosophila	670	70	6.3	267	2	Q9SHW0	Q9shw0	arabidopsis
598	70.5	6.4	1173	1	ATC2_YEAST	P38929	saccharomyc	671	70	6.3	270	2	Q9D8C2	Q9d8c2	mus musculi
599	70.5	6.4	1203	2	Q9NGZ4	Q9ngz4	drosophila	672	70	6.3	273	2	Q61Y62	Q61y62	mus musculi
600	70.5	6.4	1291	2	Q9V1F9	Q9v1f9	drosophila	673	70	6.3	281	2	P97300	Q9ep73	mus musculi
601	70.5	6.4	1788	2	Q91AJO	Q91ajo	xenopus lae	674	70	6.3	290	2	Q9EP73	Q9ep73	mus musculi
602	70.5	6.4	2607	2	Q614J5	Q614j5	solanum dem	675	70	6.3	292	2	Q97O8E	Q97o8e	streplococ
603	70.5	6.4	2672	1	GCN1_YEAST	P33892	saccharomyc	676	70	6.3	296	2	Q8DPI5	Q8dpi5	streplococ
604	70	6.4	94	2	Q9K3M7	Q9k3m7	streplococu	677	70	6.3	297	2	Q6C5D7	Q6c5d7	yarowia li
605	70	6.4	122	2	Q8C9G7	Q8c9g7	mus musculi	678	70	6.3	300	2	Q8BEKO	Q8beko	varu
606	70	6.4	183	2	Q9TQ08	Q9tq08	bos indicus	679	70	6.3	303	2	Q92RX2	Q92rx2	rhizodium m
607	70	6.4	184	2	Q9TTR5	Q9ttr5	bos taurus	680	70	6.3	307	2	Q646C7	Q646c7	pan paniscu
608	70	6.4	264	2	Q9YK85	Q9yeks	aeoropyum p	681	70	6.3	310	2	Q8BE17	Q8be17	vaccinia vi
609	70	6.4	276	2	Q6B0R7	Q6b0r7	brachydanio	682	70	6.3	315	2	Q8U6V9	Q8u6v9	agrobacteri
610	70	6.4	280	2	Q8K3G1	Q8k3g1	rattus norv	683	70	6.3	323	2	Q6F222	Q6f222	mesoplasma
611	70	6.4	302	2	Q617J2	Q617j2	lactobacill	684	70	6.3	334	1	Q6TXS0	Q6txs0	cherax dest
612	70	6.4	304	2	Q89X91	Q89x91	bradyrhizob	685	70	6.3	348	1	V1PL_HUMAN	Q910V9	homo sapien
613	70	6.4	306	2	Q634Y3	Q634y3	baillius ce	686	70	6.3	351	1	FX11_HUMAN	Q12951	homo sapien
614	70	6.4	306	2	Q730Z2	Q730z2	baillius ce	687	70	6.3	359	2	Q63HN6	Q63hn6	homo sapien
615	70	6.4	310	1	FTSX_HAEIN	P44872	haemophilus	688	70	6.3	361	2	Q8HX64	Q8hx64	sus scrofa

689	69.5	6.3	361	2	Q8MHT5	Q8mht5 sus scrofa	762	69	6.3	728	2	Q9MAQ5	Q9ma45 arabidopsis
690	69.5	6.3	361	2	Q8SPB9	Q8spb9 sus scrofa	763	69	6.3	773	2	Q9BR04	Q9br04 mycoplasma
691	69.5	6.3	395	2	Q9FKY4	Q9fky4 arabidopsis	764	69	6.3	811	1	COAT_GMDNV	Q90125 galliera me
692	69.5	6.3	406	2	Q7PPV3	Q7ppv3 anopheles g	765	69	6.3	864	2	Q6FVU1	Q6fvu1 candida gla
693	69.5	6.3	412	2	Q63611	Q63611 rattus norv	766	69	6.3	943	2	Q9FG43	Q9fg43 arabidopsis
694	69.5	6.3	412	2	Q9RIE1	Q9rie1 rattus norv	767	69	6.3	996	2	P90735	P90735 caenorhabdi
695	69.5	6.3	427	2	Q8CIE8	Q8cie8 mus musculi	768	69	6.3	996	2	Q27461	Q27461 caenorhabdi
696	69.5	6.3	446	2	Q6C008	Q6c008 mus musculi	769	69	6.3	1017	1	A1A2_CHICK	P47497 gallus gall
697	69.5	6.3	446	2	Q6C008	Q6c008 kluveromys	770	69	6.3	1059	2	Q6UXL7	Q6uxl7 homo sapien
698	69.5	6.3	450	2	Q7Y849	Q7y849 kluveromys	771	69	6.3	1119	2	Q6UXM1	Q6uxm1 homo sapien
699	69.5	6.3	450	2	Q8XCN3	Q8xcn3 geobacter s	772	69	6.3	1181	1	ITR17_HUMAN	Q13683 homo sapien
700	69.5	6.3	455	2	Q8SXY5	Q8sxy5 drosophila	773	69	6.3	1191	1	Q756U3	Q756u3 aahya goos
701	69.5	6.3	455	2	Q6AFY9	Q6afy9 leifsonia x	774	69	6.3	1256	2	Q6BT77	Q6bt77 debaryomyce
702	69.5	6.3	479	2	Q7A9A2	Q7a9a2 escherichia	775	69	6.3	1560	2	Q9GRX5	Q9grx5 dictyosteli
703	69.5	6.3	481	2	Q8X8A5	Q8x8a5 escherichia	776	69	6.3	1561	2	Q9U987	Q9u987 dictyosteli
704	69.5	6.3	490	2	Q94CC5	Q94cc5 arabidopsis	777	69	6.3	1993	2	Q7PS34	Q7ps34 anopheles g
705	69.5	6.3	552	2	Q67QA3	Q67qa3 symbiobacte	778	69	6.3	5017	2	Q81R70	Q81r70 bacillus ce
706	69.5	6.3	555	2	Q69HR1	Q69hr1 clona lites	779	69	6.3	74	2	Q8R4P1	Q8r4p1 mus musculi
707	69.5	6.3	623	2	Q9HIE1	Q9hie1 thermoplasma	780	69	6.2	110	2	Q9KZQ3	Q9kzq3 streptomyce
708	69.5	6.3	679	2	Q7R5N8	Q7r5n8 giardia lam	781	69	6.2	116	2	Q8LBX7	Q8lbx7 arabidopsis
709	69.5	6.3	708	2	Q87239	Q87239 lactococcus	782	69	6.2	140	2	Q69M00	Q69m00 oryza sativ
710	69.5	6.3	745	2	Q6DIR2	Q6dir2 xenopus tro	783	69	6.2	141	2	P91181	P91181 caenorhabdi
711	69.5	6.3	795	2	Q6C6R5	Q6c6r5 yarrowia li	784	69	6.2	179	2	Q7POH2	Q7poh2 anopheles g
712	69.5	6.3	882	2	Q9TZL6	Q9tzt6 caenorhabdi	785	69	6.2	248	2	Q62701	Q62701 sus scrofa
713	69.5	6.3	900	2	Q74925	Q74925 schizosacch	786	69	6.2	296	2	Q881P7	Q881p7 pseudomonas
714	69.5	6.3	956	2	Q8BMF5	Q8bmf5 mus musculi	787	69	6.2	304	2	Q9TQX1	Q9txq1 canis famli
715	69.5	6.3	1021	2	Q7XKA3	Q7xka3 oryza sativ	788	69	6.2	316	2	Q20259	Q20259 caenorhabdi
716	69.5	6.3	1036	1	ATHL_RAT	P54708 rattus norv	789	69	6.2	330	1	QUTG_EMENTI	P25416 emericella
717	69.5	6.3	1069	1	PCH7_HUMAN	Q60245 homo sapien	790	69	6.2	342	2	Q304F8	Q304f8 equus caball
718	69.5	6.3	1560	1	Q18291	Q18291 caenorhabdi	791	69	6.2	348	1	RNFD_VIBCH	Q9kt89 vibrio chol
719	69.5	6.3	2283	1	DPOE_MOUSE	Q9wv17 mus musculi	792	69	6.2	360	2	Q95558	Q95558 peromyscus
720	69.5	6.3	2283	1	Q80XH7	Q80xh7 mus musculi	793	69	6.2	365	2	Q93UK1	Q93uk1 burkholderi
721	69	6.3	157	2	Q7QAU5	Q7qau5 anopheles g	794	69	6.2	383	2	Q63R65	Q63r65 mus musculi
722	69	6.3	220	2	Q8KXG6	Q8kxg6 chlorobium	795	69	6.2	397	1	C244_MOUSE	Q24445 helicobacte
723	69	6.3	224	2	Q932N1	Q932n1 staphylococ	796	69	6.2	410	2	Q7MSH8	Q7msh8 porphyromon
724	69	6.3	231	2	Q9HUP0	Q9hup0 pseudomonas	797	69	6.2	417	2	Q25454	Q25454 brachydario
725	69	6.3	275	2	Q9RK73	Q9rk73 streptomyce	798	69	6.2	422	2	Q7ZT28	Q7zt28 brachydario
726	69	6.3	305	2	Q98M70	Q98m70 rhizobium l	799	69	6.2	444	2	Q8HWV8	Q8hwv8 lantana cam
727	69	6.3	321	2	Q7I2W9	Q7i2w9 listeria mo	800	69	6.2	469	2	Q18644	Q18644 caenorhabdi
728	69	6.3	332	2	Q6SLI8	Q6sl18 pollicipes	801	69	6.2	477	2	Q8M8X4	Q8m8x4 selago thom
729	69	6.3	339	2	Q9GJRO	Q9gjk0 salmo trutt	802	69	6.2	478	2	Q70IC1	Q70ic1 calceolaria
730	69	6.3	345	2	Q92215	Q92215 mus musculi	803	69	6.2	483	1	PRVB_ECOLI	P32154 escherichia
731	69	6.3	347	1	VIPL_MOUSE	P59481 mus musculi	804	69	6.2	483	1	Q7UB78	Q7ub78 shigella fl
732	69	6.3	358	2	Q93556	Q93556 carassius a	805	69	6.2	485	2	Q83PE3	P26313 junin arena
733	69	6.3	358	2	Q95559	Q95559 peromyscus	806	69	6.2	485	2	Q83PE3	Q83pe3 shigella fl
734	69	6.3	369	1	Q9PSR_ANOCA	P41592 anolis caro	807	69	6.2	485	2	O10428	O10428 junin arena
735	69	6.3	372	2	Q9D259	Q9d259 mus musculi	808	69	6.2	485	2	O10429	O10429 junin arena
736	69	6.3	390	2	Q8KR52	Q8kr52 escherichia	809	69	6.2	485	2	Q61VU3	Q61vu3 junin arena
737	69	6.3	393	2	Q7RI96	Q7ri96 plasmodium	810	69	6.2	485	2	Q6UV73	Q6uv73 junin arena
738	69	6.3	394	2	Q8IK51	Q8ik51 plasmodium	811	69	6.2	502	2	O81915	O81915 arabidopsis
739	69	6.3	395	2	Q8CGD8	Q8cgd8 mus musculi	812	69	6.2	506	2	Q7YJ21	Q7yj21 harpagophyt
740	69	6.3	398	2	Q90ZL8	Q90z18 anas platyr	813	69	6.2	511	2	Q8YV02	Q8yv02 anabaena sp
741	69	6.3	401	2	Q9KXK6	Q9kxk6 vibrio chol	814	69	6.2	522	2	O41526	O41526 canine hecp
742	69	6.3	433	2	Q8A897	Q8a897 bacteroides	815	69	6.2	522	2	Q91334	Q91334 canine hecp
743	69	6.3	454	2	Q862D2	Q862d2 fusarium ox	816	69	6.2	524	2	Q72VH1	Q72vh1 leptospira
744	69	6.3	456	2	Q643C2	Q643c2 streptomyce	817	69	6.2	524	2	Q8F9I8	Q8f9i8 leptospira
745	69	6.3	479	2	Q93JF0	Q93jfo streptomyce	818	69	6.2	531	2	Q91E38	Q91e38 phocid hecp
746	69	6.3	482	2	Q70IB8	Q70ib8 calceolaria	819	69	6.2	539	2	Q7RC79	Q7rc79 plasmodium
747	69	6.3	495	2	Q7VYL6	Q7vyl6 haemophilus	820	69	6.2	543	2	Q804X8	Q804x8 gallus gall
748	69	6.3	495	2	Q9APW3	Q9apw3 haemophilus	821	69	6.2	559	2	Q8TPP5	Q8tp5 methanosaac
749	69	6.3	501	2	Q6DBS3	Q6db53 erwina car	822	69	6.2	564	2	O81S03	O81s03 babesia bov
750	69	6.3	512	2	Q95K28	Q95k28 macaca fasc	823	69	6.2	564	2	O67184	O67184 aquilex aeo
751	69	6.3	569	2	Q73VL3	Q73vl3 mycobacteri	824	69	6.2	568	2	Q74LW5	Q74lw5 lactobacilli
752	69	6.3	616	1	NDVA_RHIME	P18767 rhizobium m	825	69	6.2	572	2	Q9VNM8	Q9vnm8 drosophila
753	69	6.3	645	2	Q6BPF6	Q6bpf6 debaryomyce	826	69	6.2	589	2	Q68X75	Q68x75 rickettsia
754	69	6.3	666	2	Q6MT84	Q6mt84 drosophila	827	69	6.2	593	2	Q68CX6	Q68cx6 streptococc
755	69	6.3	668	2	Q9V3S9	Q9v3s9 drosophila	828	69	6.2	593	2	Q8D290	Q8d290 streptococc
756	69	6.3	686	2	Q6ZFT2	Q6zft2 oryza sativ	829	69	6.2	604	1	ITAB_PAPCY	P53711 papio cynoc
757	69	6.3	697	2	Q8NC72	Q8nc72 homo sapien	830	69	6.2	645	2	Q7RJ59	Q7rj59 plasmodium
758	69	6.3	707	2	Q95JH7	Q95jh7 macaca fasc	831	69	6.2	674	2	Q7XIS7	Q7xis7 oryza sativ
759	69	6.3	723	2	Q6ZM32	Q6zm32 homo sapien	832	69	6.2	676	1	ATKB_ENTFA	Q8ku73 enterococcu
760	69	6.3	723	2	Q7Z329	Q7z329 homo sapien	833	69	6.2	698	2	Q8WY15	Q8wy15 homo sapien
761	69	6.3	723	2	Q7Z388	Q7z388 homo sapien	834	69	6.2	785	2	Q6CTN0	Q6ctn0 kluveromys

835	68.5	6.2	798	2	080G03	080g03 gallus gall	908	68	6.2	644	2	095RU0	095r0 drosophila
836	68.5	6.2	798	2	072YV7	072y7 gallus gall	909	68	6.2	664	2	095W41	095w41 arabidopsis
837	68.5	6.2	799	1	ITEN_DROME	027591 drosophila	910	68	6.2	666	2	091UD5	091ud5 arabidopsis
838	68.5	6.2	807	2	021895	021895 caenorhabd1	911	68	6.2	679	2	086Q05	086q05 anopheles g
839	68.5	6.2	831	2	069XP2	069xp2 oryza sativ	912	68	6.2	681	2	09FFW5	09ffw5 arabidopsis
840	68.5	6.2	907	2	09FLT4	09fl4 arabidopsis	913	68	6.2	691	2	022138	022138 arabidopsis
841	68.5	6.2	998	2	06G0M2	06gm2 xenopus lae	914	68	6.2	699	2	06BEN8	06ben8 pseudomonas
842	68.5	6.2	1022	2	07R0M7	07mr7 plasmodium	915	68	6.2	699	2	0600C3	0600c3 pseudomonas
843	68.5	6.2	1025	1	ADA1_YEAST	P38065 baccharomyc	916	68	6.2	699	2	06R0Z7	06r0z7 pseudomonas
844	68.5	6.2	1041	2	08X0M4	08xm4 ralsitonia s	917	68	6.2	729	1	06XDA4	06xda4 pseudomonas
845	68.5	6.2	1101	2	039157	039157 arabidopsis	918	68	6.2	802	2	06UY21	06uy21 homo sapien
846	68.5	6.2	1111	2	09FL71	09fl71 arabidopsis	919	68	6.2	803	2	08N106	08n106 homo sapien
847	68.5	6.2	1123	2	09ZIB3	09zib3 wolinnella r	920	68	6.2	802	2	08N106	08n106 homo sapien
848	68.5	6.2	1179	1	ITAE_HUMAN	P38570 wolinnella r	921	68	6.2	878	2	08YV23	08yv23 anabaena sp
849	68.5	6.2	1238	2	09ZIB5	09zib5 wolinnella r	922	68	6.2	884	1	06NTM0	06ntm0 xenopus lae
850	68.5	6.2	1269	2	081J05	081j05 plasmodium	923	68	6.2	905	1	06NTM0	06ntm0 xenopus lae
851	68.5	6.2	1305	2	0757A3	0757a3 ashbya gos	924	68	6.2	923	2	07PWA2	07pwa2 anopheles g
852	68.5	6.2	1710	2	08PSN8	08psn8 methanosarc	925	68	6.2	924	2	07PWA2	07pwa2 anopheles g
853	68.5	6.2	1776	2	06HMI2	06hmi2 debaryomyce	926	68	6.2	924	2	08LN27	08ln27 oryza sativ
854	68.5	6.2	1896	2	091AJ1	091aj1 xenopus lae	927	68	6.2	927	2	08N107	08n107 oryza sativ
855	68.5	6.2	1926	2	07S5T9	07s5t9 neurospora	928	68	6.2	973	1	UVPA_AGR15	08uf86 agrobacteri
856	68.5	6.2	145	2	09CYN8	09cyn8 mus musculu	929	68	6.2	1022	2	090WE7	090we7 catassius a
857	68.5	6.2	153	2	072J00	072j00 thermus the	930	68	6.2	1036	2	07YRP8	07yrp8 equus caball
858	68.5	6.2	168	2	09ZGF6	09zgf6 heliobacill	931	68	6.2	1137	2	086W93	086w93 homo sapien
859	68.5	6.2	171	2	069504	069504 human herpe	932	68	6.2	1231	2	06Y8G3	06y8g3 anopheles g
860	68.5	6.2	183	2	06P9G4	06p9g4 homo sapien	933	68	6.2	1223	2	07MEM3	07mem3 vibrio vuln
861	68.5	6.2	190	2	07NAX3	07nax3 mycoplasma	934	68	6.2	1227	2	06TFN4	06tfn4 canida gla
862	68.5	6.2	217	2	080V73	080v73 mus musculu	935	68	6.2	1360	2	002006	002006 drosophila
863	68.5	6.2	218	2	08BRH2	08brh2 oceanobacil	936	68	6.2	1818	2	076C94	076c94 drosophila
864	68.5	6.2	218	2	07JN61	07jn61 dictyostell	937	68	6.2	1818	2	076C95	076c95 drosophila
865	68.5	6.2	254	2	023871	023871 dictyostell	938	68	6.2	2268	2	0814N5	0814n5 plasmodium
866	68.5	6.2	267	2	08UE11	08ue11 agrobacteri	939	68	6.2	2321	1	NTC3_HUMAN	09um47 homo sapien
867	68.5	6.2	270	2	099MB6	099mb6 mus musculu	940	68	6.2	2344	2	06QW00	06qw00 rabbit hemo
868	68.5	6.2	270	2	09CQ56	09cq56 m mus muscu	941	68	6.2	2461	2	07TN88	07tn88 mus musculu
869	68.5	6.2	275	2	094BJ8	094bj8 berberidops	942	68	6.2	8094	2	081LB9	081lb9 plasmodium
870	68.5	6.2	284	2	081M26	081m26 plasmodium	943	68	6.2	16223	2	081R22	081r22 drosophila
871	68.5	6.2	290	2	08AUP3	08aup3 ptychotromis	944	68	6.2	136	2	06RGL8	06rgl8 sena alata
872	68.5	6.2	290	2	08AUP5	08aup5 haplochromi	945	68	6.2	161	2	06TLL1	06tll1 drosophila
873	68.5	6.2	290	2	08AUP5	08aup5 haplochromi	946	68	6.2	193	2	060408	060408 cavia cutle
874	68.5	6.2	290	2	08AV04	08av04 ysbichromis	947	68	6.2	206	2	08R479	08r479 mus musculu
875	68.5	6.2	291	2	06C1C6	06c1c6 kluveromyc	948	68	6.2	207	2	08YGX2	08ygx2 bruceia me
876	68.5	6.2	291	2	09W2U9	09w2u9 felis silve	949	68	6.2	207	2	08G021	08g021 arabidopsis
877	68.5	6.2	294	2	08SPW3	08spw3 macaca fasc	950	68	6.2	210	2	09FL88	09fl88 heliconius
878	68.5	6.2	297	2	092J54	092j54 rhizobium m	951	68	6.2	220	2	037488	037488 bruceia me
879	68.5	6.2	310	2	07CYK0	07cyk0 agrobacteri	952	68	6.2	227	2	09GCL6	09gcl6 seticinus m
880	68.5	6.2	318	1	YOHQ_BACSU	P54515 bacillus su	953	68	6.2	269	1	086FE2	086fe2 schistosoma
881	68.5	6.2	338	2	06DHD4	06dhd4 brachydanio	954	68	6.2	270	1	ILIA_PIG	08r430 sus scrofa
882	68.5	6.2	342	2	08YFD6	08yfd6 bruceia me	955	68	6.2	274	2	09GKD9	09gkd9 bos taurus
883	68.5	6.2	362	1	OPSR_CHICK	P22129 gallus gall	956	68	6.2	1275	2	09FZ05	09fz05 lycopersico
884	68.5	6.2	362	2	08SPC0	08spc0 sus scrofa	957	68	6.2	280	1	TNR6_RAT	09d387 rattus norv
885	68.5	6.2	397	2	0822F7	0822f7 enterococcu	958	68	6.2	283	1	CTX3_MOUSE	08d187 mus musculu
886	68.5	6.2	398	2	06D8T4	06d8t4 erylina car	959	68	6.2	283	2	08EUR1	08eur1 mycoplasma
887	68.5	6.2	399	2	07BM45	07bm45 salmonella	960	68	6.2	289	1	CYP_MASLA	08eur1 mycoplasma
888	68.5	6.2	406	2	09KIK0	09kik0 salmonella	961	68	6.2	289	1	08KFG5	P83793 maatigoclad
889	68.5	6.2	406	2	07NHJ5	07nhj5 gloeobacter	962	68	6.2	292	2	08LAG0	08kfg5 chlorobium
890	68.5	6.2	423	2	017985	017985 caenorhabd1	963	68	6.2	295	2	08OYL6	08lag0 arabidopsis
891	68.5	6.2	433	2	062254	062254 caenorhabd1	964	68	6.2	297	2	08HKB4	08oyl6 mus musculu
892	68.5	6.2	452	2	07UA98	07ua98 shigella fl	965	68	6.2	299	2	09EMK9	08hkb4 roboactra e
893	68.5	6.2	454	2	0862E4	0862e4 gibberella	966	68	6.2	312	1	LPHY_HELPJ	09emk9 amacta moo
894	68.5	6.2	472	2	0811T8	0811t8 mus musculu	967	68	6.2	320	2	08GDT5	09emb1 heliobacte
895	68.5	6.2	489	2	097CTS	097cts thermoplaam	968	68	6.2	330	2	09Z203	08gdt5 cyanidiosch
896	68.5	6.2	504	2	09X4B6	09x4b6 eschericha	969	68	6.2	351	2	0701J7	09z203 arabidopsis
897	68.5	6.2	510	2	07YK03	07ykq3 gratioli of	970	68	6.2	351	2	086SV4	0701j7 anopheles g
898	68.5	6.2	512	2	07XSP9	07xsp9 oryza sativ	971	68	6.2	356	2	06K4G2	086sv4 homo sapien
899	68.5	6.2	516	2	08ESH6	08esh6 oceanobacil	972	68	6.2	361	2	08MXG9	06k4g2 oryza sativ
900	68.5	6.2	538	2	098PI0	098pi0 mycoplasma	973	68	6.2	361	2	091E16	08mxg9 sus scrofa
901	68.5	6.2	543	1	DALS_YEAST	P15365 saccharomye	974	68	6.2	362	2	0910P9	091e16 rice black
902	68.5	6.2	544	2	061196	061196 caenorhabd1	975	68	6.2	362	2	08B4T7	0910p9 rice black
903	68.5	6.2	570	2	09NKH8	09nkh8 drosophila	976	68	6.2	370	1	C244_HUMAN	08b4t7 rice black
904	68.5	6.2	587	2	06HSF8	06hsf8 bacillus an	977	68	6.2	378	1	YF69_AQUAB	09nkh8 homo sapien
905	68.5	6.2	587	2	081L02	081l02 bacillus an	978	68	6.2	387	2	017845	06hsf8 caenorhabd1
906	68.5	6.2	587	2	06HCJ3	06hcj3 bacillus th	979	68	6.2	399	2	022079	022079 caenorhabd1
907	68.5	6.2	592	2	09N618	09n618 drosophila	980	68	6.2	423	2	09UYP7	09uyp7 pyrococcus

981	67.5	6.1	425	2	Q9BL95	Q9b195 caenorhabdi	1054	67	6.1	157	2	Q66x97	Q66x97 hesperia co
982	67.5	6.1	428	2	Q8M968	Q8m968 proboscidea	1055	67	6.1	178	2	Q6CWP0	Q6cwp0 kluyverimyc
983	67.5	6.1	431	2	Q7RLQ4	Q7rlq4 plasmodium	1056	67	6.1	194	2	Q8LZR9	Q8lzt9 gymnomleu
984	67.5	6.1	437	2	Q6FKB2	Q6fkb2 candida gla	1057	67	6.1	215	2	Q9BKZ8	Q9bkz8 caenorhabdi
985	67.5	6.1	447	2	Q9PHJ1	Q9phj1 xyloella fas	1058	67	6.1	220	1	CD28_HUMAN	PI0747 homo sapien
986	67.5	6.1	468	2	Q9RWV3	Q9rwv3 deinococcus	1059	67	6.1	223	2	Q8K8J7	Q8k8j7 streptococc
987	67.5	6.1	472	2	Q23699	Q23699 arabidopsis	1060	67	6.1	234	2	Q70W60	Q70w60 homo sapien
988	67.5	6.1	475	2	Q8VDD8	Q8vdd8 mus musculu	1061	67	6.1	259	2	Q9NZ43	Q9nz43 homo sapien
989	67.5	6.1	478	2	Q6AVE3	Q6ave3 oryza sativ	1062	67	6.1	261	1	PEF4_HUMAN	Q13156 homo sapien
990	67.5	6.1	479	2	Q94KD9	Q94kd9 arabidopsis	1063	67	6.1	290	2	Q8AUN1	Q8aun1 paralabidoc
991	67.5	6.1	481	2	Q8M970	Q8m970 peltanthera	1064	67	6.1	290	2	Q8AUR6	Q8aur6 ysaichromis
992	67.5	6.1	486	2	Q45749	Q45749 caenorhabdi	1065	67	6.1	297	2	Q9VFR0	Q9vfr0 drosophila
993	67.5	6.1	489	2	Q9A762	Q9a762 caulobacter	1066	67	6.1	304	2	Q20961	Q20961 caenorhabdi
994	67.5	6.1	494	2	Q7ZTK1	Q7ztk1 xenopus lae	1067	67	6.1	304	2	Q9F4C1	Q9f4c1 bacillus me
995	67.5	6.1	496	2	Q8AZ57	Q8az57 machupo vir	1068	67	6.1	305	2	Q6NBO3	Q6nb03 rhodospseudo
996	67.5	6.1	497	2	Q9LMM7	Q9lmm7 arabidopsis	1069	67	6.1	306	2	Q81ZU0	Q81zu0 bacillus ce
997	67.5	6.1	500	2	Q7YKM5	Q7ykm5 proboscidea	1070	67	6.1	309	2	Q58296	Q58296 pyrococcus
998	67.5	6.1	505	2	Q9Y799	Q9y799 candida par	1071	67	6.1	328	2	Q8M020	Q8m020 methanococc
999	67.5	6.1	507	2	Q66K78	Q66k78 homo sapien	1072	67	6.1	329	2	Q8W3Y0	Q8w3y0 citrus jamb
1000	67.5	6.1	508	2	Q9T162	Q9t162 hemimeris s	1073	67	6.1	333	2	Q8CT52	Q8ct52 staphylococ
1001	67.5	6.1	533	2	Q65JM8	Q65jm8 bacillus li	1074	67	6.1	350	1	Q6S0L7	Q6s0l7 bos taurus
1002	67.5	6.1	539	2	Q8G559	Q8g559 bifidobacte	1075	67	6.1	352	2	Q6S0L7	Q6s0l7 bacteroides
1003	67.5	6.1	540	2	Q6NMR2	Q6nmr2 homo sapien	1076	67	6.1	353	2	Q8HX43	Q8hx43 salmo salar
1004	67.5	6.1	543	2	Q6CBN8	Q6cbn8 yarrowia li	1077	67	6.1	354	2	Q72D61	Q72d61 desulfovibr
1005	67.5	6.1	561	2	Q8M234	Q8m234 drosophila	1078	67	6.1	355	2	Q8HX44	Q8hx44 salmo salar
1006	67.5	6.1	570	2	Q6GJX3	Q6gjx3 staphylococ	1079	67	6.1	357	2	Q76DX8	Q76dx8 plecoglossu
1007	67.5	6.1	589	2	Q6P4C8	Q6p4c8 homo sapien	1080	67	6.1	359	2	Q9W771	Q9w771 colomba liv
1008	67.5	6.1	589	2	Q7PB25	Q7pb25 rickettsia	1081	67	6.1	364	1	QPSR_HUMAN	P94000 homo sapien
1009	67.5	6.1	589	2	Q921Y4	Q921y4 rickettsia	1082	67	6.1	366	2	Q9N3J4	Q9n3j4 clostridium
1010	67.5	6.1	607	2	Q8K217	Q8k217 mus musculu	1083	67	6.1	378	2	Q951P5	Q951p5 strizobedio
1011	67.5	6.1	608	1	Y093_METUA	Q8f788 methanococc	1084	67	6.1	379	2	Q6BPL6	Q6bpl6 debaryomyce
1012	67.5	6.1	612	1	LEM2_MOUSE	Q00690 mus musculu	1085	67	6.1	386	2	Q63BG1	Q63bg1 bacillus ce
1013	67.5	6.1	622	1	Q91570	Q91570 xenopus lae	1086	67	6.1	400	2	Q8CSE4	Q8cse4 mus musculu
1014	67.5	6.1	656	2	SL54_MOUSE	Q9act37 mus musculu	1087	67	6.1	406	2	Q9OAT4	Q9oat4 african swi
1015	67.5	6.1	657	2	Q93127	Q93127 spodoptera	1088	67	6.1	413	1	Q6KDB4	P22519 escherichia
1016	67.5	6.1	666	2	Q9XED4	Q9xed4 phascolus v	1089	67	6.1	413	2	Q6KDB4	Q6kdb4 escherichia
1017	67.5	6.1	669	2	Q6ARX9	Q6etr9 desulfotale	1090	67	6.1	413	2	Q9RPH4	Q9rph4 mycobacteri
1018	67.5	6.1	689	2	Q74AA9	Q74aa9 geobacter s	1091	67	6.1	415	2	Q73AC4	Q73ac4 bacillus ce
1019	67.5	6.1	724	2	Q96GR2	Q96gr2 homo sapien	1092	67	6.1	418	2	Q766V2	Q766v2 gallus gall
1020	67.5	6.1	724	2	Q9HC26	Q9hc26 homo sapien	1093	67	6.1	424	1	MCHE_ECOLI	Q8exn6 escherichia
1021	67.5	6.1	729	2	Q76N27	Q76n27 homo sapien	1094	67	6.1	424	2	Q83Z98	Q83z98 escherichia
1022	67.5	6.1	730	2	Q8MX65	Q8mx65 homo sapien	1095	67	6.1	424	2	Q83ZAS	Q83zas escherichia
1023	67.5	6.1	735	2	Q9LMP2	Q9lmp2 oryza sativ	1096	67	6.1	424	2	Q841V2	Q841v2 escherichia
1024	67.5	6.1	750	2	Q91838	Q91838 xenopus lae	1097	67	6.1	424	2	Q8F1X7	Q8f1x7 escherichia
1025	67.5	6.1	827	2	Q80M06	Q80m06 mus musculu	1098	67	6.1	437	2	Q7M8Y7	Q7m8y7 wolinnella s
1026	67.5	6.1	827	2	Q8B7J0	Q8b7j0 mus musculu	1099	67	6.1	445	2	Q8HVV4	Q8hvv4 cleroendru
1027	67.5	6.1	854	2	Q6MYT3	Q6myt3 aaspergillus	1100	67	6.1	446	2	Q6ES01	Q6es01 olkopleura
1028	67.5	6.1	915	2	Q7SBE9	Q7sbe9 neurospora	1101	67	6.1	447	2	Q8HVX3	Q8hvx3 cleroendru
1029	67.5	6.1	915	2	Q7SBE2	Q7sbe2 neurospora	1102	67	6.1	447	2	Q64Y00	Q64y00 bacteroides
1030	67.5	6.1	1035	2	Q9M7U0	Q9m7j0 populus tre	1103	67	6.1	452	2	Q83RZ4	Q83rz4 shigella fl
1031	67.5	6.1	1048	2	Q92T03	Q92t03 rhizobium m	1104	67	6.1	457	2	Q8ZB93	Q8zb93 yersinia pe
1032	67.5	6.1	1049	2	Q9AUT8	Q9aut8 oryza sativ	1105	67	6.1	477	2	Q8CYN0	Q8cyn0 streptococc
1033	67.5	6.1	1053	1	ITAS_MOUSE	PI1668 mus musculu	1106	67	6.1	477	2	Q8DOH7	Q8doh7 yersinia pe
1034	67.5	6.1	1053	2	Q80YF5	Q80yp5 mus musculu	1107	67	6.1	479	2	Q98S64	Q98s64 guillardia
1035	67.5	6.1	1078	2	Q7Y010	Q7y010 oryza sativ	1108	67	6.1	491	2	Q6C1G6	Q6c1g6 yarrowia li
1036	67.5	6.1	1222	2	Q86HL6	Q86hl6 dictyosteli	1109	67	6.1	496	2	Q7NAZ6	Q7naz6 photorhabd
1037	67.5	6.1	1222	2	Q86SA4	Q86sa4 dictyosteli	1110	67	6.1	504	2	Q8SN35	Q8sn35 diplopanax
1038	67.5	6.1	1313	2	Q723Y0	Q723y0 listeria mo	1111	67	6.1	506	2	Q85480	Q85480 helicobacte
1039	67.5	6.1	1375	2	Q8ML47	Q8ml47 drosophila	1112	67	6.1	509	2	Q995C5	Q995c5 pitfall vir
1040	67.5	6.1	1375	2	Q94537	Q94537 drosophila	1113	67	6.1	512	1	FIOL_RAT	Q995c5 ratius norv
1041	67.5	6.1	1523	2	Q7RS28	Q7rs28 plasmodium	1114	67	6.1	512	2	Q9QUM8	Q9qum8 rattus norv
1042	67.5	6.1	1526	2	Q94538	Q94538 drosophila	1115	67	6.1	513	2	Q8RC50	Q8rc50 thermoaer
1043	67.5	6.1	1894	2	Q9V6D5	Q9v6d5 drosophila	1116	67	6.1	518	2	Q8MPX9	Q8mpx9 caenorhabdi
1044	67.5	6.1	1912	1	Q64487	Q64487 mus musculu	1117	67	6.1	556	2	Q22938	Q22938 caenorhabdi
1045	67.5	6.1	1912	1	PRPD_HUMAN	P23468 homo sapien	1118	67	6.1	566	2	Q8PL71	Q8pl71 xanthomonas
1046	67.5	6.1	2066	2	P88930	P88930 cat blue dw	1119	67	6.1	585	2	Q69JG2	Q69jg2 oryza sativ
1047	67.5	6.1	2720	2	Q8IP64	Q8ip64 drosophila	1120	67	6.1	591	2	Q22271	Q22271 caenorhabdi
1048	67.5	6.1	2771	2	Q9VL63	Q9vl63 drosophila	1121	67	6.1	605	2	Q6GNL9	Q6gnl9 xenopus lae
1049	67.5	6.1	3665	2	Q7UQ60	Q7uq60 rhodopirell	1122	67	6.1	648	2	Q7KWN1	Q7kwn1 dictyosteli
1050	67.5	6.1	4834	2	Q95714	Q95714 homo sapien	1123	67	6.1	650	2	Q9SKL8	Q9skl8 arabidopsis
1051	67	6.1	43	1	P79464	P79464 bos taurus	1124	67	6.1	673	2	Q9W10	Q9w10 drosophila
1052	67	6.1	95	2	PXY6_HUMAN	P90nc03 homo sapien	1125	67	6.1	701	1	HRPH_PSESX	Q01723 pseudomonas
1053	67	6.1	120	2	Q6UW52	Q6uw52 homo sapien	1126	67	6.1	705	2	Q85969	Q85969 sphingomona



1127	67	6.1	714	2	Q6ZPE6	Q6ZPE6 mus musculus	1200	66.5	6.0	415	2	Q8A718	Q8A718 bacteroides
1128	67	6.1	720	2	Q4O902	Q4O902 pecunia int	1201	66.5	6.0	419	1	Q8A566	Q8A566 streptococc
1129	67	6.1	730	2	Q8D9P1	Q8D9P1 vibrio vuln	1202	66.5	6.0	419	1	Q8K5G6	Q8K5G6 streptococc
1130	67	6.1	782	2	Q18654	Q18654 caenorhabdi	1203	66.5	6.0	419	2	Q8NKK1	Q8NKK1 streptococc
1131	67	6.1	790	2	Q94GL4	Q94GL4 oryza sativ	1204	66.5	6.0	422	2	Q6QAN7	Q6QAN7 carassius a
1132	67	6.1	803	2	Q6P9F7	Q6P9F7 homo sapien	1205	66.5	6.0	423	2	Q8N2D4	Q8N2D4 homo sapien
1133	67	6.1	829	1	CADG_HUMAN	Q75309 homo sapien	1206	66.5	6.0	425	2	Q18923	Q18923 caenorhabdi
1134	67	6.1	836	2	Q9V3Q9	Q9V3Q9 dirosophila	1207	66.5	6.0	439	2	Q9H2V8	Q9H2V8 homo sapien
1135	67	6.1	840	2	Q9BML7	Q9BML7 dirosophila	1208	66.5	6.0	439	2	Q7R2R8	Q7R2R8 leptoepira
1136	67	6.1	842	2	Q83XL3	Q83XL3 legionella	1209	66.5	6.0	441	2	Q816B9	Q816B9 bacillus ce
1137	67	6.1	868	2	Q9SDN6	Q9sdn6 nicotiana t	1210	66.5	6.0	442	2	Q9BY67	Q9BY67 homo sapien
1138	67	6.1	906	1	CADO_XENLA	P33147 xenopus lae	1211	66.5	6.0	443	2	Q6VLX3	Q6VLX3 mus musculu
1139	67	6.1	956	1	GUK4_FAT	Q01812 rattus norv	1212	66.5	6.0	444	1	QX2R_HUMAN	Q43614 mus saplen
1140	67	6.1	1009	2	Q9U458	Q9U458 dirosophila	1213	66.5	6.0	444	2	Q632FL	Q632f1 bacillus ce
1141	67	6.1	1017	2	Q9OX34	Q9OX34 brachydanto	1214	66.5	6.0	444	2	Q72YH1	Q72YH1 bacillus ce
1142	67	6.1	1017	2	Q9DGL5	Q9dgl5 brachydanto	1215	66.5	6.0	444	2	Q81K62	Q81K62 bacillus ce
1143	67	6.1	1023	1	ALAI_BUFMA	P30714 bufo marinu	1216	66.5	6.0	444	2	Q6HBZ4	Q6hbz4 bacillus th
1144	67	6.1	1023	1	ALAI_OREMO	Q9YH26 oreochromis	1217	66.5	6.0	445	2	Q8K3T6	Q8K3t6 mus musculu
1145	67	6.1	1024	2	Q9OX33	Q9OX33 brachydanto	1218	66.5	6.0	445	2	Q8R4L1	Q8r4l1 mus musculu
1146	67	6.1	1024	2	Q9DEU0	Q9deu0 brachydanto	1219	66.5	6.0	460	1	QX2R_MOUSE	P58308 mus musculu
1147	67	6.1	1032	1	ALIA_MOUSE	Q94W27 mus musculu	1220	66.5	6.0	460	1	QX2R_RAT	P56719 rattus norv
1148	67	6.1	1034	2	Q9TUN4	Q9tun4 oryctolagus	1221	66.5	6.0	468	2	Q9NZL2	Q9nzl2 homo sapien
1149	67	6.1	1117	2	Q6P1C6	Q6p1c6 mus musculu	1222	66.5	6.0	482	1	MURE_AQUAE	Q67631 aquifex aeo
1150	67	6.1	1127	2	Q7R5V0	Q7r5v0 giardia lam	1223	66.5	6.0	485	2	Q8BSB5	Q8bsb5 lactobacill
1151	67	6.1	1139	2	Q8D7L5	Q8d7l5 vibrio vuln	1224	66.5	6.0	489	1	YHIP_ECOLI	P36837 escherichia
1152	67	6.1	1348	2	Q2S199	Q2s199 hydra atcen	1225	66.5	6.0	489	2	Q8FCL2	Q8fcl2 escherichia
1153	67	6.1	1361	1	MER_YEAST	Q04693 saccharomyc	1226	66.5	6.0	489	2	Q8X5O8	Q8x5o8 escherichia
1154	67	6.1	1382	1	RSEI_RAT	P97523 rattus norv	1227	66.5	6.0	496	2	Q81UF7	Q81uf7 machupo vir
1155	67	6.1	1529	2	Q67VX5	Q67vx5 oryza sativ	1228	66.5	6.0	496	2	Q6LVU5	Q6lvu5 machupo vir
1156	67	6.1	1556	2	Q9M159	Q9m159 dirosophila	1229	66.5	6.0	496	2	Q6PXP4	Q6pXP4 machupo vir
1157	67	6.1	1593	2	Q8T6H1	Q8t6h1 dictyosteli	1230	66.5	6.0	510	2	Q9SJO8	Q9sjo8 arabidopsis
1158	67	6.1	1829	2	Q61VD6	Q61vd6 strongyloce	1231	66.5	6.0	512	2	Q6ZFP3	Q6zfp3 oryza sativ
1159	66.5	6.0	108	2	Q6S7D7	Q6s7d7 sus scrofa	1232	66.5	6.0	518	1	BHE2_HUMAN	Q97520 homo sapien
1160	66.5	6.0	135	2	Q9K8Z2	Q9k8z2 bacillus ha	1233	66.5	6.0	518	2	Q85IK9	Q85ik9 beta vulgar
1161	66.5	6.0	155	2	Q64F76	Q64f76 lactococcus	1234	66.5	6.0	523	2	Q6BYQ4	Q6byq4 debaryomyce
1162	66.5	6.0	155	2	Q64F79	Q64f79 lactococcus	1235	66.5	6.0	529	2	Q7NNH4	Q7nnh4 gloeobacter
1163	66.5	6.0	155	2	Q64F77	Q64f77 lactococcus	1236	66.5	6.0	534	2	Q8OZV1	Q8ozv1 rattus norv
1164	66.5	6.0	155	2	Q64F83	Q64f83 lactococcus	1237	66.5	6.0	536	2	Q8KG54	Q8kg54 chlorobium
1165	66.5	6.0	208	2	Q6BYV4	Q6byv4 schistosoma	1238	66.5	6.0	539	2	Q8CFW3	Q8cfw3 mus musculu
1166	66.5	6.0	223	2	Q88GV3	Q88gv3 dirosophila	1239	66.5	6.0	558	2	Q8T4C6	Q8t4c6 dirosophila
1167	66.5	6.0	231	1	HGXR_PLAFK	P07833 plasmodium	1240	66.5	6.0	568	2	Q6KXY3	Q6kxy3 plerophyllus
1168	66.5	6.0	268	2	Q9EP57	Q9ep57 mus musculu	1241	66.5	6.0	571	2	Q576Q4	Q576q4 gallus gall
1169	66.5	6.0	268	2	Q9J1O1	Q9j1o1 mus musculu	1242	66.5	6.0	600	2	Q86BE1	Q86be1 dirosophila
1170	66.5	6.0	270	2	Q6SWS0	Q6swo0 human cytom	1243	66.5	6.0	603	2	Q7KRC4	Q7krC4 dirosophila
1171	66.5	6.0	271	2	Q6DGI9	Q6dgi9 brachydanto	1244	66.5	6.0	606	2	Q8DMG6	Q8dmg6 synchococc
1172	66.5	6.0	273	2	Q9JMA4	Q9jma4 mus musculu	1245	66.5	6.0	612	2	Q7X6Q8	Q7x6q8 leptoepira
1173	66.5	6.0	274	2	Q8BJ59	Q8bj59 mus musculu	1246	66.5	6.0	712	2	Q7X6Q8	Q7x6q8 oryza sativ
1174	66.5	6.0	281	2	Q9J1O2	Q9j1o2 mus musculu	1247	66.5	6.0	721	2	Q6DDN6	Q6ddn6 xenopus lae
1175	66.5	6.0	285	2	Q87UH6	Q87uh6 pseudomomas	1248	66.5	6.0	729	2	Q8LB06	Q8lb06 arabidopsis
1176	66.5	6.0	289	2	Q6GP29	Q6gp29 xenopus lae	1249	66.5	6.0	733	2	Q9FKQ8	Q9fkq8 arabidopsis
1177	66.5	6.0	295	2	Q9Z2H8	Q9z2h8 mus musculu	1250	66.5	6.0	757	2	Q82L71	Q82l71 streptomyc
1178	66.5	6.0	307	2	Q645U6	Q645u6 pongo pygma	1251	66.5	6.0	777	2	Q6BG55	Q6bg55 parametium
1179	66.5	6.0	309	2	Q646A0	Q646a0 gorilla gor	1252	66.5	6.0	830	1	NMT1_SCHPO	Q02592 schizosacch
1180	66.5	6.0	318	2	Q6ZEV0	Q6zev0 burkholderi	1253	66.5	6.0	830	2	Q665G7	Q665g7 yersinia ps
1181	66.5	6.0	318	2	Q6ZYD3	Q6zyd3 burkholderi	1254	66.5	6.0	830	2	Q6ODZ2	Q6odz2 yersinia ps
1182	66.5	6.0	325	2	Q02838	Q02838 sus scrofa	1255	66.5	6.0	837	2	Q6FZA3	Q6fza3 bartonella
1183	66.5	6.0	356	2	Q8HX66	Q8hx66 sus scrofa	1256	66.5	6.0	964	2	Q821Q4	Q821q4 streptomyc
1184	66.5	6.0	361	2	Q8MGT8	Q8mgts sus scrofa	1257	66.5	6.0	973	2	Q7Q438	Q7q438 anopheles g
1185	66.5	6.0	361	2	Q8MGT5	Q8mgt5 sus scrofa	1258	66.5	6.0	1030	2	Q17443	Q17443 caenorhabdi
1186	66.5	6.0	364	2	Q19245	Q19245 sus scrofa	1259	66.5	6.0	1081	2	Q76809	Q76809 hydra atcen
1187	66.5	6.0	364	2	Q8MHU4	Q8mhu4 sus scrofa	1260	66.5	6.0	1088	2	Q9XX01	Q9xx01 caenorhabdi
1188	66.5	6.0	364	2	Q31068	Q31068 sus scrofa	1261	66.5	6.0	1119	2	Q86G88	Q86g88 pseudoplusii
1189	66.5	6.0	366	2	Q8BV78	Q8bv78 mus musculu	1262	66.5	6.0	1136	2	Q8EUT8	Q8eut8 caenorhabdi
1190	66.5	6.0	366	2	Q31069	Q31069 sus scrofa	1263	66.5	6.0	1200	2	Q6CJF8	Q6cjf8 kluyveromyc
1191	66.5	6.0	369	2	Q84EK9	Q84ek9 shewanella	1264	66.5	6.0	1210	2	Q7Y719	Q7y719 caenorhabdi
1192	66.5	6.0	378	2	Q81642	Q81642 plasmodium	1265	66.5	6.0	1349	2	Q9ZEV6	Q9zev6 listeria in
1193	66.5	6.0	390	2	Q8PMN2	Q8pmn2 mechanosarc	1266	66.5	6.0	1406	2	Q01777	Q01777 caenorhabdi
1194	66.5	6.0	390	2	Q7PQJ8	Q7pqj8 anopheles g	1267	66.5	6.0	1522	2	Q756Z0	Q756z0 anhyva goss
1195	66.5	6.0	393	1	PKRI_HUMAN	Q8ctw9 homo sapien	1268	66.5	6.0	1542	2	Q7KVP4	Q7kvp4 dirosophila
1196	66.5	6.0	395	2	Q877M4	Q877m4 streptococc	1269	66.5	6.0	1546	2	Q86BS7	Q86bs7 dirosophila
1197	66.5	6.0	400	2	Q54867	Q54867 streptococc	1270	66.5	6.0	1629	2	Q9W2H8	Q9w2h8 dirosophila
1198	66.5	6.0	403	2	Q7NFO1	Q7nfo1 gloeobacter	1271	66.5	6.0	1687	2	Q7Q1M9	Q7q1m9 anopheles g
1199	66.5	6.0	404	2	Q54866	Q54866 streptococc	1272	66.5	6.0	1697	2	Q7RT82	Q7rte2 plasmodium

1273	66.5	6.0	1729	2	Q7SCY4	Q7scy4 neurospora	1346	66	6.0	480	2	O65483	O65483 arabidopsis
1274	66.5	6.0	1770	1	R115 YEAST	P43565 saccharomyc	1347	66	6.0	482	2	O66AC0	O66ac0 yersinia ps
1275	66.5	6.0	1821	2	O9ROC4	O9roc4 mus musculu	1348	66	6.0	495	2	O6CCJ3	O6ccj3 yarrowia li
1276	66.5	6.0	2013	2	O8VHZ8	O8vhz8 rattus norv	1349	66	6.0	503	1	VGJY_PIRARV	P03540 pichinde ar
1277	66.5	6.0	2013	2	O9ERC8	O9erc8 mus musculu	1350	66	6.0	508	2	O11957	O11957 pichinde ar
1278	66.5	6.0	2231	2	O7SEK8	O7sek8 ashbya goss	1351	66	6.0	508	2	O11998	O11998 pichinde ar
1279	66.5	6.0	2325	2	O9N3X8	O9n3x8 caenorhabdi	1352	66	6.0	509	2	O94AR8	O94a8 arabidopsis
1280	66.5	6.0	2799	1	G112 HUMAN	O61zfe homo sapien	1353	66	6.0	509	2	O9TOL4	O9tol4 arabidopsis
1281	66.5	6.0	3069	2	O702P4	O702p4 homo sapien	1354	66	6.0	509	2	O11999	O11999 pichinde ar
1282	66.5	6.0	3135	2	O709D0	O709d0 homo sapien	1355	66	6.0	526	1	CEA1_HUMAN	P13668 homo sapien
1283	66.5	6.0	3174	1	V13A_HUMAN	O6er17 homo sapien	1356	66	6.0	526	2	O701F1	Q701f1 fusarium pr
1284	66.5	6.0	4803	2	O84BC7	O84bc7 histococ sp.	1357	66	6.0	532	2	O8WUV6	Q8wuv6 homo sapien
1285	66	6.0	128	2	O6NDN8	O6ndn8 rhodospoedo	1358	66	6.0	532	2	O8EOY3	Q8eoy3 oceanobacil
1286	66	6.0	167	2	O82UD2	O82ud2 nitrosomona	1359	66	6.0	532	2	O8EZU8	Q8ezu8 leptospira
1287	66	6.0	179	2	O9TXU1	O9txu1 caenorhabdi	1360	66	6.0	539	2	O9MB11	Q9mb11 arabidopsis
1288	66	6.0	193	1	V319_MYCPN	P75329 mycoplasma	1361	66	6.0	572	2	P71187	P71187 enterobacte
1289	66	6.0	206	2	O72MT3	O72mt3 leptospira	1362	66	6.0	573	2	O23530	Q23530 caenorhabdi
1290	66	6.0	223	2	O8P1L8	O8p1l8 streptococc	1363	66	6.0	605	2	O6UVY4	Q6uvy4 homo sapien
1291	66	6.0	223	2	O9AOK2	O9aok2 streptococc	1364	66	6.0	605	2	O9N253	Q9n253 homo sapien
1292	66	6.0	226	1	R446_SCHPO	O42894 schizosacch	1365	66	6.0	620	2	O9NEG8	Q9neg8 leishmania
1293	66	6.0	247	2	O9KJ13	O9kji3 yersinia en	1366	66	6.0	623	2	O23521	Q23521 arabidopsis
1294	66	6.0	248	2	O96J10	O96j10 homo sapien	1367	66	6.0	631	2	P71143	P71143 clostridium
1295	66	6.0	251	2	O7POX7	O7pox7 chromobacte	1368	66	6.0	652	2	O7VN07	Q7vn07 haemophilus
1296	66	6.0	252	1	KSGA_MYCPU	O981j3 mycoplasma	1369	66	6.0	653	1	LR4_HUMAN	Q7hbw1 homo sapien
1297	66	6.0	252	2	O68X29	O68x29 rickettsia	1370	66	6.0	654	1	P57A_MYCGE	P47651 mycoplasma
1298	66	6.0	253	2	O62323	O62323 mus musculu	1371	66	6.0	698	1	ALT_BPT2	Q38424 bacterioph
1299	66	6.0	257	2	O7NCK6	O7ncx6 glaeobacter	1372	66	6.0	705	2	O9UIX2	Q9uix2 homo sapien
1300	66	6.0	260	2	O9XWS8	O9xws8 caenorhabdi	1373	66	6.0	710	2	O9M0H1	Q9moh1 arabidopsis
1301	66	6.0	260	2	O8XX82	O8xx82 ralsconia s	1374	66	6.0	718	2	O38887	Q38887 arabidopsis
1302	66	6.0	267	2	O8XS82	O8xs82 archaeglob	1375	66	6.0	726	2	O6FXV8	Q6fxv8 candida gla
1303	66	6.0	268	2	O8NQ71	O8nq71 corynebacte	1376	66	6.0	730	2	O7MKR2	Q7mkp2 vibrio vuln
1304	66	6.0	268	2	O8G877	O8g877 bifidobacte	1377	66	6.0	735	2	O64505	Q64505 arabidopsis
1305	66	6.0	275	2	O9F102	O9f102 arabidopsis	1378	66	6.0	748	2	O6DRC2	Q6drc2 brachydanio
1306	66	6.0	277	2	O7WNL8	O7wnl8 bordetella	1379	66	6.0	782	2	O9H9V8	Q9h9v8 homo sapien
1307	66	6.0	284	2	O9PU52	O9pu52 campylobact	1380	66	6.0	782	2	O8X6V4	Q8x6v4 escherichia
1308	66	6.0	298	2	O8KYN2	O8kyn2 bacillus an	1381	66	6.0	782	2	O9Z1H6	Q9z1h6 mus musculu
1309	66	6.0	298	2	O6EZR6	O6ezr6 bacillus an	1382	66	6.0	782	2	O8VDF2	Q8vdf2 mus musculu
1310	66	6.0	299	2	O73S22	O73s22 mycobacteri	1383	66	6.0	784	2	O7XLR6	Q7xlr6 oryza sativ
1311	66	6.0	307	2	O61Y2	O61y2 bacillus an	1384	66	6.0	786	2	O73W24	Q73w24 mycobacteri
1312	66	6.0	308	2	O8U1T4	O8u1t4 agrobacteri	1385	66	6.0	798	2	O9GLP0	Q9glp0 sus scrofa
1313	66	6.0	317	2	O9D3N6	O9d3n6 mus musculu	1386	66	6.0	798	2	O6P4X1	Q6p4x1 xenopus tro
1314	66	6.0	327	2	O7TRQ9	O7trq9 mus musculu	1387	66	6.0	820	2	O6D0P8	Q6d0p8 erwiniia car
1315	66	6.0	328	2	O7D1Y6	O7d1y6 agrobacteri	1388	66	6.0	830	2	O81MA0	Q81ma0 homo sapien
1316	66	6.0	328	2	O7VA71	O7va71 prochlorococ	1389	66	6.0	835	2	O6DCP0	Q6dcp0 xenopus lae
1317	66	6.0	328	2	O9W11	O9w11 bovine herp	1390	66	6.0	901	2	O8GDJ9	Q8gdj9 photorhabd
1318	66	6.0	331	2	O704Z8	O704z8 rubus idaeu	1391	66	6.0	946	2	O9L796	Q9l796 arabidopsis
1319	66	6.0	332	2	O6DYN2	O6dyn2 triops long	1392	66	6.0	956	1	G1K4_HUMAN	Q16099 homo sapien
1320	66	6.0	334	2	O6ZK97	O6zkr97 homo sapien	1393	66	6.0	1076	1	RPOB_ASTLO	P27059 ascastia ion
1321	66	6.0	338	2	O6H1G1	O6h1g1 bacillus th	1394	66	6.0	1115	1	ITAJ_DROME	O44366 drosophila
1322	66	6.0	340	2	O9BHL2	O9bhl2 caenorhabdi	1395	66	6.0	1117	2	O89ZX4	Q89zx4 bacteroides
1323	66	6.0	341	2	O87531	O87531 streptococc	1396	66	6.0	1155	2	O7OF51	Q7of51 anopheles g
1324	66	6.0	341	2	O7CMM6	O7cmm6 streptococc	1397	66	6.0	1166	2	O91AS7	Q91as7 agrobacteri
1325	66	6.0	343	2	O7QCT9	O7qct9 anopheles g	1398	66	6.0	1330	2	O6CHC3	Q6chc3 yarrowia li
1326	66	6.0	345	2	O7P3R6	O7p3r6 fusobacteri	1399	66	6.0	1372	2	O6FMR4	Q6fmr4 candida gla
1327	66	6.0	357	1	OPSR_ASTFA	P22332 actyanax fa	1400	66	6.0	1401	1	O7KWQ9	Q7kwq9 dictyosteli
1328	66	6.0	361	2	O9A1A7	O9a1a7 nicotiana t	1401	66	6.0	1536	1	SIN3_YEAST	P22579 saccharomyc
1329	66	6.0	362	2	O81JY1	O81jy1 plasmodium	1402	66	6.0	1726	2	O6XHB2	Q6xhb2 dictyosteli
1330	66	6.0	362	2	O951T0	O951t0 trichosurus	1403	66	6.0	2089	2	O9M067	Q9m067 arabidopsis
1331	66	6.0	364	2	O9XSX3	O9xsx3 macaca fasc	1404	66	6.0	2160	2	O17709	Q17709 caenorhabdi
1332	66	6.0	365	2	O20731	O20731 caenorhabdi	1405	66	6.0	2322	2	O8MDY4	Q8mdy4 rabbit hemo
1333	66	6.0	365	2	O9Y152	O9y152 ambystoma t	1406	66	6.0	3207	2	O8MWQ3	Q8mwq3 plasmodium
1334	66	6.0	368	2	O64RH0	O64rhn0 bacteroides	1407	66	6.0	3283	2	O7RP14	Q7rp14 plasmodium
1335	66	6.0	384	1	PKR2_BOVIN	O8epn1 bos taurus	1408	66	6.0	3738	2	O65645	Q65645 arabidopsis
1336	66	6.0	384	1	PKR2_HUMAN	O6nf16 homo sapien	1409	66	6.0	82	2	O8RAP3	Q8rap3 mus musculu
1337	66	6.0	393	1	PKR1_BOVIN	O8epn2 bos taurus	1410	66	5.9	110	2	O7VB08	Q7vbd8 prochloroc
1338	66	6.0	411	2	O871F7	O871f7 vibrio para	1411	66	5.9	145	2	O9U120	Q9u120 homo sapien
1339	66	6.0	413	2	O8XFG0	O8xfg0 salmonella	1412	66	5.9	149	1	YB29_MYCPN	P75346 mycoplasma
1340	66	6.0	413	2	O7CP73	O7cp73 salmonella	1413	66	5.9	155	2	O860J1	Q860j1 giraffa cam
1341	66	6.0	445	2	O9NUN2	O9nunj2 endeis laev	1414	66	5.9	155	2	O64F78	Q64f78 lactococcus
1342	66	6.0	450	2	O95BP9	O95bp9 trichoplila	1415	66	5.9	157	2	O7Z548	Q7z548 homo sapien
1343	66	6.0	452	2	O8ZVR8	O8zvr8 pyrobaculum	1416	66	5.9	166	2	O7Z548	Q7z548 homo sapien
1344	66	6.0	453	2	O9PUY6	O9pyu6 chlamydia m	1417	66	5.9	192	2	O8ZNO1	Q8zn01 salmonella
1345	66	6.0	477	2	O97066	O97q66 streptococc	1418	66	5.9	215	1	RAN_BRUMA	P38542 druglia mala

1419	65.5	5.9	216	2	0812L5	0812L5 plasmidium
1420	65.5	5.9	218	2	Q7NMB5	Q7NMB5 gloeobacter
1421	65.5	5.9	220	2	Q66176	Q66176 agrobacteri
1422	65.5	5.9	220	2	Q7D2P8	Q7D2P8 agrobacteri
1423	65.5	5.9	227	2	Q13513	Q13513 homo sapien
1424	65.5	5.9	229	2	Q63549	Q63549 drosophila
1425	65.5	5.9	231	2	081JSL	081JSL plasmidium
1426	65.5	5.9	243	2	Q9UEB4	Q9UEB4 homo sapien
1427	65.5	5.9	269	2	Q95297	Q95297 homo sapien
1428	65.5	5.9	271	2	Q9LRE6	Q9LRE6 arabidopsis
1429	65.5	5.9	273	2	Q6DUV0	Q6DUV0 mus musculu
1430	65.5	5.9	279	2	Q7TST0	Q7TST0 mus musculu
1431	65.5	5.9	285	1	FCG2_RAT	FCG203 rattus norv
1432	65.5	5.9	292	2	Q9FY94	Q9FY94 arabidopsis
1433	65.5	5.9	294	2	Q9MZV0	Q9MZV0 canis fami1
1434	65.5	5.9	298	2	Q8K319	Q8K319 mus musculu
1435	65.5	5.9	298	2	Q804R4	Q804R4 brachydanio
1436	65.5	5.9	309	2	Q645T5	Q645T5 macaca mula
1437	65.5	5.9	309	2	Q646G1	Q646G1 papio hamad
1438	65.5	5.9	311	1	Q1J1_CANFA	Q9154 canis fami1
1439	65.5	5.9	315	2	Q9UJ37	Q9UJ37 caenorhabdi
1440	65.5	5.9	330	2	Q8WKA7	Q8WKA7 drosophila
1441	65.5	5.9	330	2	Q9VPS8	Q9VPS8 drosophila
1442	65.5	5.9	331	2	Q9XV83	Q9XV83 caenorhabdi
1443	65.5	5.9	338	2	Q7NJ10	Q7NJ10 gloeobacter
1444	65.5	5.9	344	2	Q6P6J9	Q6P6J9 mus musculu
1445	65.5	5.9	348	2	Q94T19	Q94T19 caelotrichu
1446	65.5	5.9	349	2	Q6LP34	Q6LP34 photobacter
1447	65.5	5.9	352	2	Q8MHT1	Q8MHT1 sus scrofa
1448	65.5	5.9	352	2	Q8SP46	Q8SP46 sus scrofa
1449	65.5	5.9	352	2	Q8SP47	Q8SP47 sus scrofa
1450	65.5	5.9	352	2	Q8SPB0	Q8SPB0 sus scrofa
1451	65.5	5.9	359	2	Q7XQP4	Q7XQP4 oryza sativ
1452	65.5	5.9	360	2	Q8SPB8	Q8SPB8 sus scrofa
1453	65.5	5.9	361	2	Q19075	Q19075 sus scrofa
1454	65.5	5.9	361	2	Q8HX69	Q8HX69 sus scrofa
1455	65.5	5.9	361	2	Q8HMT7	Q8HMT7 sus scrofa
1456	65.5	5.9	361	2	Q8MHT9	Q8MHT9 sus scrofa
1457	65.5	5.9	361	2	Q8SPC1	Q8SPC1 sus scrofa
1458	65.5	5.9	361	2	Q86OV1	Q86OV1 sus scrofa
1459	65.5	5.9	363	1	Q86OV2	Q86OV2 sus scrofa
1460	65.5	5.9	363	1	LEU3_SALT1	Q82311 salmonella
1461	65.5	5.9	363	2	Q7KTM4	Q7KTM4 drosophila
1462	65.5	5.9	364	2	Q19243	Q19243 sus scrofa
1463	65.5	5.9	364	2	Q8SPC2	Q8SPC2 sus scrofa
1464	65.5	5.9	364	2	Q86OU6	Q86OU6 sus scrofa
1465	65.5	5.9	364	2	Q86OU9	Q86OU9 sus scrofa
1466	65.5	5.9	364	2	Q41525	Q41525 canine hepr
1467	65.5	5.9	367	2	Q9GIW7	Q9GIW7 ictalurus p
1468	65.5	5.9	369	2	Q8BV80	Q8BV80 mus musculu
1469	65.5	5.9	372	2	Q9OY50	Q9OY50 brachydanio
1470	65.5	5.9	374	2	Q7VSK4	Q7VSK4 bordelella
1471	65.5	5.9	374	2	Q7W2T8	Q7W2T8 bordelella
1472	65.5	5.9	374	2	Q7WDT6	Q7WDT6 bordelella
1473	65.5	5.9	383	2	Q7TIC0	Q7TIC0 brachydanio
1474	65.5	5.9	403	2	Q6NZV3	Q6NZV3 brachydanio
1475	65.5	5.9	414	2	Q7RRC9	Q7RRC9 plasmidium
1476	65.5	5.9	417	2	P72520	P72520 streptococ
1477	65.5	5.9	417	2	Q8A7J2	Q8A7J2 bacteroides
1478	65.5	5.9	435	2	Q45851	Q45851 caenorhabdi
1479	65.5	5.9	443	2	Q8HVX8	Q8HVX8 avicennia m
1480	65.5	5.9	443	2	Q71KM2	Q71KM2 avicennia m
1481	65.5	5.9	444	2	QX2R_CANFA	Q9CUP7 canis fami1
1482	65.5	5.9	450	2	Q04601	Q04601 arabidopsis
1483	65.5	5.9	452	2	Q7V2G4	Q7V2G4 saccharomyc
1484	65.5	5.9	476	1	YQ32_YEAST	YQ3270 saccharomyc
1485	65.5	5.9	479	2	Q8AYW1	Q8AYW1 guaranitico v
1486	65.5	5.9	482	1	VGLY_TACV7	P31842 tacaribe vi
1487	65.5	5.9	485	2	Q65475	Q65475 arabidopsis
1488	65.5	5.9	488	2	Q7UM74	Q7UM74 rhodospirill
1489	65.5	5.9	492	2	Q8R3T2	Q8R3T2 mus musculu
1490	65.5	5.9	501	2	Q9AY46	Q9AY46 oryza sativ
1491	65.5	5.9	506	1	SHS1_BOVIN	Q46631 bos taurus

1492	65.5	5.9	507	2	Q8W4G6	Q8W4G6 arabidopsis
1493	65.5	5.9	508	2	Q90423	Q90423 pichinde ar
1494	65.5	5.9	508	2	Q9YTW9	Q9YTW9 pichinde ar
1495	65.5	5.9	508	2	Q9YTX1	Q9YTX1 pichinde ar
1496	65.5	5.9	509	2	Q766U5	Q766U5 avicennia m
1497	65.5	5.9	509	2	Q7YKM2	Q7YKM2 torenia vag
1498	65.5	5.9	513	2	Q8SM19	Q8SM19 tetranema m
1499	65.5	5.9	516	2	Q6CKH4	Q6CKH4 kluyveromyc
1500	65.5	5.9	521	2	Q96RMO	Q96RMO guillardia

## ALIGNMENTS

## RESULT 1

ID	Q6UW07	PRELIMINARY;	PRT;	212 AA.
AC	Q6UW07;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	NX-17.			
GN	ORFNames=UNQ678;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bruhn J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Haldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Hwang L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wiand P., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI)", a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL: AY359060; AAQ69419.1; -			
SQ	SEQUENCE 212 AA; 24024 MW; COAB61BA40BC315 CRC64;			
Query Match	100.0%; Score 1102; DB 2; Length 212;			
Best Local Similarity	100.0%; Pred. No. 2,4e-93;			
Matches 212; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MMLLPLVLTATIAELCOGPAENAKFKRLSIRTLALGDQAYAMDTEETLFFKMAVAFSRRK 60			
DB	1 MMLLPLVLTATIAELCOGPAENAKFKRLSIRTLALGDQAYAMDTEETLFFKMAVAFSRRK 60			
QY	61 VNNREATEISHVLGNVQVSVFVVTIDPSKNHTLPAVEVQSAIRMNKNRINNAFFPLND 120			
DB	61 VNNREATEISHVLGNVQVSVFVVTIDPSKNHTLPAVEVQSAIRMNKNRINNAFFPLND 120			
QY	121 QTLFELKIPSTLAPMDSVPPIWIIIFGVIFCIIVAIALLISGIWRRRRKKEPSVD 180			
DB	121 QTLFELKIPSTLAPMDSVPPIWIIIFGVIFCIIVAIALLISGIWRRRRKKEPSVD 180			
QY	181 DAEDKCEMNTIENGIPSDPLDMKGLIMMPS 212			
DB	181 DAEDKCEMNTIENGIPSDPLDMKGLIMMPS 212			
RESULT 2				
ID	Q9HBJ8	PRELIMINARY;	PRT;	222 AA.
AC	Q9HBJ8;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Collectrin (Transmembrane protein 27).  
GN Name=TMEM27;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21264468; PubMed=11278314; DOI=10.1074/jbc.M006723200;  
RA Zhang H., Wada J., Hida K., Tsuchiyama Y., Hitzeguchi K., Shikata K.,  
Wang H., Lin S., Kanwar Y.S., Makino H.;  
RT "Collectrin, a collecting duct-specific transmembrane glycoprotein, is  
RT a novel homolog of ACE2 and is developmentally regulated in embryonic  
RT kidneys".  
RL J. Biol. Chem. 276.17132-17139 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow, Colon, and Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,  
Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,  
Kryzwiniski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
Jones S.J., Maiz M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RA Straube R.L.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Straube R.L.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Straube R.L.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF229179; AAG09466.1; -;  
DR EMBL; BC014317; AAH14317.1; -;  
DR EMBL; BC015099; AAH15099.1; -;  
DR EMBL; BC050606; AAH50606.1; -;  
DR GO: GO:0016021; C: integral to membrane; IEA.  
KW Transmembrane.  
SQ SEQUENCE 222 AA; 2535 MW; 52C0ED522134ED05 CRC64;  
Query Match 97.4%; Score 1073; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1,2e-99;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 VPNEATEISHVLLCNCVTVQVRSFVVTDPSSKNTLPAVEVQSAIRNMKRRINNAFFLND 120  
QY 121 QTLEFLKIPSTLAPMPDPSVPIWIIIFGVIFCIITVAALLISGIMQRRKNKPESEVD 180  
DB 121 QTLEFLKIPSTLAPMPDPSVPIWIIIFGVIFCIITVAALLISGIMQRRKNKPESEVD 180  
QY 181 DAEDKCNMTIENGIPSDPLDMKGG 206  
DB 181 DAEDKCNMTIENGIPSDPLDMKGG 206  
RESULT 3  
ID 06AYY2 PRELIMINARY; PRT; 222 AA.  
AC 06AYY2;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Kidney-specific membrane protein.  
DE Name=Nkx17;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,  
Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,  
Kryzwiniski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
Jones S.J., Maiz M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Director AGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC078838; AAH78838.1; -;  
SQ SEQUENCE 222 AA; 25051 MW; 82716CBF4B689778 CRC64;  
Query Match 84.8%; Score 935; DB 2; Length 222;  
Best Local Similarity 85.4%; Pred. No. 6.1e-78;  
Matches 176; Conservative 13; Mismatches 17; Indels 0; Gaps 0;



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Db      61 VPNEATEISHVLLCNITQVRSFWFVVTDPSSNNYTLPAEVOQSAIRKRNKRINSAPFLDD 120
Qy      121 QTEFLKIPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIWRRKRNKEPSEVD 180
Db      121 HTLEFLKIPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIWRRKRNKEPSEVD 180
Qy      181 DAEDKCNMTITENGIPSPDPLDMKGG 206
Db      181 DAEDKCNMTITENGIPSPDPLDMKGG 206

RESULT 5
Q9ESG3 PRELIMINARY; PRT; 222 AA.
ID Q9ESG3
AC Q9ESG3
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Collectrin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RC MEDLINE=9362608; PubMed=10432394;
RA Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hirasuhi K., Hida K.,
RA Shikata K., Makino H.,
RT "Screening for genes up-regulated in 5/6 nephrectomized mouse
RT kidney.";
RL Kidney Int. 56:549-558(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RC MEDLINE=21264468; PubMed=11278314; DOI=10.1074/jbc.M006723200;
RA Zhang H., Wada J., Hida K., Tsuchiyama Y., Hirasuhi K., Shikata K.,
RA Wang H., Lin S., Kanwar Y.S., Makino H.;
RT "Collectrin, a collecting duct-specific transmembrane glycoprotein, is
RT a novel homolog of ACE2 and is developmentally regulated in embryonic
RT kidney.";
RL J. Biol. Chem. 276:17132-17139(2001).
DR EMBL; AF178086; AAG09307.1; -.
SQ SEQUENCE 222 AA; 25226 MW; 7FAE166AE344F855 CRC64;

Query March 83.6%; Score 921; DB 2; Length 222;
Best Local Similarity 84.5%; Pred. No. 1.2e-76;
Matches 174; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy      1 MLWLLFLVTAIHAEELCPGAEAFKVRSLIRITLGDKAYAMDNEEYLFKAMVAFSMRK 60
Db      1 MLWLLFLVTTIHAEELCPDAENAFKVRSLIKALGDKAYAMDNEEYLFAMVAFSMRK 60
Qy      61 VPNEARETISHVLLCNVTVQVRSFWFVVTDPKSHHTLPAVEVOQSAIRKRNKRINNAFFLND 120
Db      61 VPNEGEETISHVLLCNVTVQVRSFWFVVTDPKSHHTFPAVEVOQSAIRKRNKRINNAFFLDD 120
Qy      121 QTEFLKIPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIWRRKRNKEPSEVD 180
Db      121 HTLEFLKIPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIWRRKRNKEPSEVD 180
Qy      181 DAEDKCNMTITENGIPSPDPLDMKGG 206
Db      181 DAEDKCNMTITENGIPSPDPLDMKGG 206

RESULT 6
Q6PE94 PRELIMINARY; PRT; 228 AA.
ID Q6PE94
AC Q6PE94
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

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DE      MGC68634 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Rana S.S., Luquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058203; AAH58203.1; -.
SQ SEQUENCE 228 AA; 25224 MW; 3A16B4B027E2E7E2 CRC64;

Query March 44.3%; Score 488; DB 2; Length 228;
Best Local Similarity 47.2%; Pred. No. 9.4e-37;
Matches 93; Conservative 47; Mismatches 55; Indels 2; Gaps 2;

Qy      1 MLWLLFLVTAIHAEELCPGAEAFKVRSLIRITLGDKAYAMDNEEYLFKAMVAFSMRK 60
Db      5 ILFLFLPFTVHDDLPDPSRGALKVRINIKALGNATYWNDEEYLFAMVAFSMRS 64
Qy      61 VPNEARETISHVLLCNVTVQVRSFWFVVTDPGSKHHTLPAVEVOQSAIRKRNKRINNAFFLN 119
Db      65 YTKNDTQISIVTVCNSTERVSFWFVVTSPENSHPVSYSEVAVNEBRRINSAPFLN 124
Qy      120 QTEFLKIPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIWRRKRNKEPSEVD 178
Db      125 DKTLEFQIIPPTLAPASQSSSSSWLVGVVFAVVAIALVLSGIRRRKRLKSSEE 184
Qy      179 VDAEDKCNMTITENG 195
Db      185 SQNSEARMSGLDAIKNG 201

RESULT 7
Q6PO50 PRELIMINARY; PRT; 235 AA.
ID Q6PO50
AC Q6PO50
DT 05-JUL-2004 (Tremblrel. 27, Created)

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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE LOC0402976 protein (Fragment).
GN Name=LOC0402976;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OK NCBI_TaxId=955;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RX MEDLINE=2228657; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopline R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullins S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RA Struhsberg R.;
RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC065470; AAH65470.1; -.
FT NON_TER 1
SQ SEQUENCE 235 AA; 26152 MW; FB09C5A64D3BC2 CRC64;

Query Match
Best Local Similarity 40.1%; Score 405; DB 2; Length 235;
Matches 83; Conservative 50; Mismatches 70; Indels 4; Gaps 3;

QY 2 LMLFFLVTAIHAEICOGCAENAFVRLSIRFALGDKAYAMDNEEYLFKAVAFSMKRV 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DT 18 LITLILPVPVADQCKE-SKDGFKVRLSLKLTALNDANENESKFLFRSLAYAMRXK 76
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 PNRKATEISHVLICNVTORVSWFVYVTPDS-KNHTLPAAVEVQSAIRNKNRINNAFPLND 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 TGEDVYNIENILVNCNDTKVSEFIPVVTLPADPTOLIPKEVEVRAVROSRRINNAFLLSD 136
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 QTLLEFLKIPSTLAPMDSEVPIMIIIFGVIFCIIVALLISGIWMORRRKNKSPSEVD 180
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 MTLFVGVPTLAVPIQNTPPMLIVFGVIGIVAVGIALMSTVSKRRKAKADAGPD 196
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 DAEDKCNMTIENGIPSDPLDMKGI 207
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 197 --QDGDDEGIVKENGALSGLNKKDGV 221
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
Q9UF26 PRELIMINARY; PRT; 804 AA.
AC Q9UF26;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp344A014 (Fragment).
GN Name=DKFZp344A014;
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Mamut R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL, AL110224; CAB3682.1; -.
DR PIR, T14762; T14762.
DR HSSP, Q10714; IJ37.
DR MEROPS, M02.006; -.
DR GO, GO:0016020; C-membrane; IEA.
DR GO, GO:0004246; F-peptidyl-dipeptidase A activity; IEA.
DR GO, GO:0006508; F-proteolysis and peptidolysis; IEA.
DR InterPro, IPR001548; Peptidase M2.
DR InterPro, IPR006025; Pept M2n BS.
DR Pfam, PF01401; Peptidase M2; 1.
DR PRINTS, PR00791; PEPTIDPASA.
DR PRODOM, PD004184; Peptidase M2; 1.
DR PROSITE, PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;

Query Match
Best Local Similarity 47.9%; Score 376; DB 2; Length 804;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAENAFVRLSIRFALGDKAYAMDNEEYLFKAVAFSMR----KVENREAT-EISHVL 73
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 611 PYADOSIVRSLKSLGDKAYEMNDNEMYLFRSSVAAMQYFLKVNQMLPDEEDVR 670
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 74 LCVTORVSWFVYVTPDSK-NHTLPAAVEVQSAIRNKNRINNAFPLNDQTLFELKIPSTL 132
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 671 VANLKRISFNFPVAPKGVSDIIPREVEKAIKRSRINDAFRLNDSLEFLGIQPTL 730
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 APPMPSVPIMIIIFGVIFCIIVALLISGIWMORRRKNKSPS 177
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 731 GPNPQPVSIWLVFGVGVAVGIVLIFLTGIRDRKKKAKRS 775
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
Q9NRA7 PRELIMINARY; PRT; 805 AA.
AC Q9NRA7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Angiotensin converting enzyme-like protein (Angiotensin I converting
DE enzyme (peptidyl-dipeptidase A) 2) (angiotensin converting enzyme 2)
DB Name=ACE2;
GN Name=ACE2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RX MEDLINE=20517872; PubMed=10924499; DOI=10.1074/jbc.M002615200;
RA Tipnis S.R., Hooper N.M., Hyde R., Karran E., Christie G.,
RA Turner A.V.;
RT "A human homolog of angiotensin-converting enzyme. Cloning and
RT functional expression as a captopril-insensitive carboxypeptidase.";
RL J. Biol. Chem. 275:33238-33243 (2000).
RN (2)
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahern M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.

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RP SEQUENCE FROM N.A.
RA Douglas G.C., O'Bryan M.K., Hedger M.P., Yarski M.A., Smith A.I.,
RA Lew R.A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20429895; PubMed=10969042;
RA Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,
RA Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
RA Breitbart R.E., Acton S.;
RT "A novel angiotensin-converting enzyme-related carboxypeptidase (ACE2)
RT converts angiotensin I to angiotensin 1-9.";
RL Cite. Res. 87:E1-E9(2000).
DR EMBL; AF241254; AAF78220.1; -
DR EMBL; AY217547; AA025651.1; -
DR EMBL; AF21820; AAF9721.1; -
DR HSSP; Q10714; 1037.
DR MEROPS; M02.006; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIP7A5A.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Carboxypeptidase.
SQ SEQUENCE 805 AA; 92462 MW; 8BE6E0A931550E8 CRC64;

Query March 34.1%; Score 376; DB 2; Length 805;
Best Local Similarity 47.9%; Pred. No. 8.3e-26;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKRLSIRLTALGDKAYAMDTEBYLFKAMVAFSMR----KYPNREAT-EISHVL 73
DB 612 PYAQDSIKVRLSLKSLGADKAYENNDNEMYLFRSSVAYARQYLFKYNQILFGSEEDVR 671
QY 74 LCNTQKVSFWFVVTDPDK-NHTLPAYEVQSAIRMKRINNAFLNDQTEFLKIPSTL 132
DB 672 VANLKPRISFNFVFTAPKNSVDILPRTEVEKAIKRSRINDARLNDNSLEFLGIPTL 731
QY 133 APPMDSPVPIWIIIFGVIFCIIVAIALLISGIWQRKKKKEPS 177
DB 732 GPNQPPVSIWLVFGVMGVIVGIVILFTGIRDRKKKKKKS 776

RESULT 10
O86WTO PRELIMINARY; PRT; 816 AA.
AC O86WTO;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ACE2 Protein (Fragment).
GN Name=ACE2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feinsold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stiplicon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleja U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC048094; AA048094.1; -
DR PDB; 1R42; X-ray; A=-.
DR PDB; 1R4L; X-ray; A=12-626.
DR MEROPS; M02.006; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIP7A5A.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 816 AA; 93516 MW; EFBBD58B3DAZEDF3 CRC64;

Query March 34.1%; Score 376; DB 2; Length 816;
Best Local Similarity 47.9%; Pred. No. 8.4e-26;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKRLSIRLTALGDKAYAMDTEBYLFKAMVAFSMR----KYPNREAT-EISHVL 73
DB 623 PYAQDSIKVRLSLKSLGADKAYENNDNEMYLFRSSVAYARQYLFKYNQILFGSEEDVR 682
QY 74 LCNTQKVSFWFVVTDPDK-NHTLPAYEVQSAIRMKRINNAFLNDQTEFLKIPSTL 132
DB 683 VANLKPRISFNFVFTAPKNSVDILPRTEVEKAIKRSRINDARLNDNSLEFLGIPTL 742
QY 133 APPMDSPVPIWIIIFGVIFCIIVAIALLISGIWQRKKKKEPS 177
DB 743 GPNQPPVSIWLVFGVMGVIVGIVILFTGIRDRKKKKKKS 787

RESULT 11
O9BYF1 PRELIMINARY; PRT; 805 AA.
AC O9BYF1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ACE2.
GN Name=ace2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Suzuki Y., Watanabe M., Sugano S.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RA Komatsu T., Suzuki Y., Sugano S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046569; BAB40370.1; -.

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DR HSSP: Q10714; 1J37.
DR MEROPS; M02.006; -.
DR Genew; HGNC:13557; ACE2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDPTASEA.
DR Prodom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR SEQUENCE 805 AA; 92490 MW; DZAAB4C2708BEB72 CRC64;

Query Match 33.8%; Score 373; DB 2; Length 805;
Best Local Similarity 47.3%; Pred. No. 1.6e-25;
Matches 78; Conservative 33; Mismatches 48; Indels 6; Gaps 3;

QY 19 PAENAFKVRSLIRTLGDKAYAMDNEEYLFKAVYAFPMR-----VPRREAT-EISHTL 73
DB 612 PYADQSIKVRISLTKSALGANAYEMTNNEFLFRSSVAYAMRYFSIIKNQTVPFLE---- 671
QY 74 LCNVTQVRSFVFVYTDPSK-NHTLPAVEVQSAIRNNKRIINNAFFPLNDQTLSEFLKIPSTL 132
DB 672 VANLKPRISEFVTPAKVSDIIPRTVEKAIIRMSRRIINAFRLNDSLEFLGIQPTL 731
QY 133 APPMDPSVPIIIIFGVIFCIITVAIALILSGIWRKKKEPS 177
DB 732 GPPNPVPSIWLIVFGVMGVIVGIVILFTGIRDKKKKKKARS 776

RESULT 12
Q8R010 PRELIMINARY; PRT; 805 AA.
AC Q8R010;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Age2 protease.
GN Name=Age2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matsuna K., Farmer A.A., Rubin G.M., Hong L.,
RA Stalcen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek U.A., Gunnarone P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumet J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC026801; AAH26801.1; -.
DR HSSP: Q10714; 1J37.
DR MEROPS; M02.006; -.
DR MGD; MGI:1917258; Ace2.
DR GO; GO:0006515; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDPTASEA.
DR Prodom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS006478; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR SEQUENCE 805 AA; 92367 MW; D8B883AAC96A8D9 CRC64;

Query Match 32.8%; Score 361; DB 2; Length 805;
Best Local Similarity 40.9%; Pred. No. 2e-24;
Matches 81; Conservative 35; Mismatches 52; Indels 30; Gaps 5;

QY 19 PAENAFKVRSLIRTLGDKAYAMDNEEYLFKAVYAFPMR-----VPRREATI 69
DB 612 PYADQSIKVRISLTKSALGANAYEMTNNEFLFRSSVAYAMRYFSIIKNQTVPFLE---- 667
QY 70 SHVLNCNTQVRSFVFVYTDPSK-NHTLPAVEVQSAIRNNKRIINNAFFPLNDQTLSEFLKI 128
DB 668 EDVRSDDLKPRSEFVFVTSFQNSVDVLRSEVEDAIRSRIRINDVFEPLNLSLEPLGI 727
QY 129 PSTLAPMDPSVPIIIIFGVIFCIITVAIALILSGIWRKKKEPS 188
DB 728 HPTLPPVPPPTIWLIIIFGVMAVVGIIILITGIGRKKKKEPTRE----- 777
QY 189 MTTENGIPSDPLDMKG 206
DB 778 ----EN--PYDSMDIGKG 789

RESULT 13
Q9D836 PRELIMINARY; PRT; 265 AA.
AC Q9D836;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Mus musculus adult male small intestine cDNA, RIKEN full-length
DE enriched library, clone:2010305L05 product:ANIGOTENSIN-CONVERTING
DE ENZYME-RELATED CARBOXYPEPTIDASE, full insert sequence.
GN Name=Age2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA The FANTOM Consortium;
the RIKEN Genome Exploration Research Group Phase I & II Team;

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RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RT Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA Adachi U., Aizawa K., Akahira S., Akimura T., Arai A., Kono H.,
RA Arahawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuo M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirao T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shnegawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa M., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK008530; BAB25723.2; -.
DR HSSP; Q10714; 1037.
DR MEROPS; M02.006; -.
DR MCD; MGI:1917258; Ace2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; 1.
DR Carboxypeptidase.
KM NON TER
FT SEQUENCE 265 AA; 30078 MW; 2A02BCE3817C76C CRC64;

Query Match 32.4%; Score 357; DB 2; Length 265;
Best Local Similarity 44.1%; Pred. No. 1.3e-24;
Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;

QY 19 PGAENAFKVRISITATGDKAYADNTNEVLFKAMVAFSMRK-----VPPREATEI 69
DB 72 PYAQOSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMKRYSIINQVTFPLE---- 127
QY 70 SHVLICVTVQVSFWFVTVDPK-NHTLPAVEVOSAIRMNKRNINNAFFLNDOTLEFLKI 128
DB 128 EDVAVSDLKPRVSYFFVTSFQNVSDVIPRSEVEDAIRMSGRINDVGLNDSLEFLGI 187
QY 129 PSTLAPPMDSVPPIWIIIFGVIFCIIVAILLISGIWRRRKKEPSE 178
DB 188 HPTLEPPYQPVVTIWLIFGVVALVVGIIILVTGIGKRRKKNETKRE 237

RESULT 14
Q99N71
Q99N71

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ID Q99N71 PRELIMINARY; PRT; 798 AA.
AC Q99N71;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Angiotensin-converting enzyme-related carboxypeptidase.
GN Name=Ace2; Synonyms=ACE2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22375506; PubMed=12487024;
RA Komatsu T., Suzuki Y., Imai J., Sugano S., Hida M., Tanigami A.,
RA Muroi S., Yamada Y., Hanaoka K.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase
RT (mACE2)."
RL DNA Seq. 13:217-220(2002).
DR EMBL; AB053181; BAB40431.1; -.
DR HSSP; Q10714; BAB40431.1; -.
DR MEROPS; M02.006; -.
DR MCD; MGI:1917258; Ace2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR006025; Pept_M2n_BS.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPTASEA.
DR PRODOM; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KM Carboxypeptidase.
SQ SEQUENCE 798 AA; 91943 MW; 403ABE29D55725A4 CRC64;

Query Match 32.4%; Score 357; DB 2; Length 798;
Best Local Similarity 44.1%; Pred. No. 4.6e-24;
Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;

QY 19 PGAENAFKVRISITATGDKAYADNTNEVLFKAMVAFSMRK-----VPPREATEI 69
DB 612 PYAQOSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMKRYSIINQVTFPLE---- 667
QY 70 SHVLICVTVQVSFWFVTVDPK-NHTLPAVEVOSAIRMNKRNINNAFFLNDOTLEFLKI 128
DB 668 EDVAVSDLKPRVSYFFVTSFQNVSDVIPRSEVEDAIRMSGRINDVGLNDSLEFLGI 727
QY 129 PSTLAPPMDSVPPIWIIIFGVIFCIIVAILLISGIWRRRKKEPSE 178
DB 728 HPTLEPPYQPVVTIWLIFGVVALVVGIIILVTGIGKRRKKNETKRE 777

RESULT 15
Q81A08
Q81A08 PRELIMINARY; PRT; 1053 AA.
ID Q81A08;
AC Q81A08;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vacuolar proton-translocating ATPase subunit A, putative.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrett B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL644507; CAD51303.1; -.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO: 0015992; P: proton transport; IEA.  
DR InterPro; IPR002490; V\_ATPase\_sub16.  
DR Pfam; PF01496; V\_ATPase\_1; 1.  
SQ SEQUENCE 1053 AA; 122998 MW; 8B9F2559D3FC3F08 CRC64;

Query Match 9.1%; Score 100; DB 2; Length 1053;  
Best Local Similarity 21.3%; Pred. No. 3;

Matches 43; Conservative 31; Mismatches 72; Indels 56; Gaps 8;

QY 22 ENAFVRLSIRFALGDKAYAMDNEEYLFKAMVAFSMRKVPNREATEISHVLLC----- 75  
DB 330 EHAKEKRIKELREIINDKEKALKAYEEYFINEIFVLINVEPNKNSLIBEWKLFCKKERHI 389  
QY 76 -----NTQRVSEFWFVVTDDPSK-NHTLPAYEVQSAIRMKKGRINNAFFLNDQTL- 123  
DB 390 YNNLNVFEGSDITLRCDWCWYSANDEKIRHIL-----INKSSNDLVSAALLSDKILR 441  
QY 124 -----EFLK-----IPSTLAP-----MDPSVPIMI---IIFGVIF-----CI 153  
DB 442 PNVSEPTIYIKTNEFTKSYQSMVDYGVPRYGEINPAISTITITPPFLFGIMYGVGHGICI 501  
QY 154 IIVAIALILSGIWQRRRNKE 175  
DB 502 FLFALFLIIMNNKVKNNKNNNE 523

Search completed: August 18, 2005, 17:37:39  
Job time : 224 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2005, 17:28:18 ; Search time 16 Seconds  
(without alignments)  
1274.872 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102  
Sequence: 1 MLMLLFLVTAIHAEICQPG.....ENGIPSDPLDMKGILMPS 212

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	376	34.1	804	2 T14762	hypothetical prote
2	97.5	8.8	1086	2 T18523	integrin alpha cha
3	94	8.5	704	2 T29996	hypothetical prote
4	92.5	8.4	1153	2 T31080	nitric-oxide synth
5	89.5	8.1	244	2 E86471	unknown protein (i
6	89.5	8.1	793	2 D38992	cadherin 8 - human
7	89.5	8.1	1188	2 T13933	pol polypeptid
8	89	8.1	1054	2 UC7294	alpha integrin -
9	88	8.0	363	2 A37009	CD44 homolog membr
10	88	8.0	365	2 A34424	CD44 membrane gly
11	86	7.8	362	2 A35616	T-cell surface gly
12	86	7.8	503	2 B38745	cell adhesion mole
13	85.5	7.8	667	2 T47482	receptor-like prot
14	84.5	7.7	468	2 E81924	probable two-compo
15	84.5	7.7	536	2 UG0022	flagellar basal-bo
16	84.5	7.7	1112	2 T28082	hypothetical prote
17	84	7.6	428	2 T48167	hypothetical prote
18	83.5	7.5	1337	1 T38670	protein-tyrosine-p
19	83	7.5	525	2 B83957	flagellar basal-bo
20	82.5	7.5	1044	2 S16516	integrin alpha-8 c
21	81.5	7.4	252	2 T05813	hypothetical prote
22	81.5	7.4	1048	2 A27421	integrin alpha-5 c
23	81	7.4	1041	2 T31437	integrin alpha cha
24	80.5	7.3	1135	2 T61186	integrin alpha-7 c
25	80.5	7.3	1034	2 A36108	integrin alpha-V c
26	80	7.3	234	1 A08E43	membrane antigen g
27	80	7.3	489	2 AF2970	conserved hypochet
28	80	7.3	489	2 D98312	hypothetical prote
29	79.5	7.2	1044	2 T10050	integrin alpha-v c

30	79	7.2	437	2 S73284	hypothetical prote
31	79	7.2	2029	1 TDBFLK	protein-tyrosine-p
32	78.5	7.1	548	2 F71732	ABC transporter At
33	78.5	7.1	836	2 T08424	tweety protein - F
34	78	7.1	343	2 A35639	G protein-coupled
35	78	7.1	377	2 AE0715	probable membrane
36	78	7.1	732	1 IJCCHB	B-cadherin precurs
37	78	7.1	1022	2 S49127	Na+/K+-exchanging
38	77.5	7.0	351	2 S45305	CD44 antigen precu
39	77.5	7.0	370	2 H64545	lipopolysaccharide
40	77.5	7.0	468	2 G81180	sensor histidine k
41	77.5	7.0	1499	2 I50212	protein-tyrosine-p
42	77	7.0	322	2 S75428	UDP-N-acetylglucos
43	77	7.0	366	2 A69063	O-antigen transpor
44	77	7.0	541	2 D97322	probable membrane-
45	77	7.0	1045	2 D97322	integrin alpha v c
46	77	7.0	180	2 A72758	hypothetical prote
47	76	6.9	306	2 D90519	hypothetical prote
48	76	6.9	369	2 H90587	hypothetical prote
49	76	6.9	542	2 T39474	amino acid permeas
50	76	6.9	614	2 B63332	conserved hypochet
51	76	6.9	771	2 T26176	hypothetical prote
52	76	6.9	1337	2 T38949	hypothetical prote
53	76	6.9	2251	2 T24490	hypothetical prote
54	76	6.9	2344	2 S64740	genome polypeptid
55	75.5	6.9	230	2 AF2237	hypothetical prote
56	75.5	6.9	255	1 S48146	hypothetical prote
57	75.5	6.9	407	2 T08732	hypothetical prote
58	75.5	6.9	549	1 H65214	probable Na+/H+ ex
59	75.5	6.9	653	2 T25194	hypothetical prote
60	75.5	6.9	1344	1 A35175	mucin 1 precursor,
61	75	6.8	1007	2 PN0156	glutamate receptor
62	75	6.8	1008	2 S28858	glutamate receptor
63	74.5	6.8	549	2 C68100	hypothetical prote
64	74.5	6.8	549	2 G91259	hypothetical prote
65	74.5	6.8	631	2 I52257	episialin - mouse
66	74.5	6.8	664	2 T47481	receptor-like prot
67	74.5	6.8	2244	2 F90563	hypothetical prote
68	74	6.7	357	2 D45229	opsin, red-sensiti
69	74	6.7	589	2 F70033	glucan 1,4-alpha-m
70	73.5	6.7	321	2 A11243	B. subtilis yqno p
71	73.5	6.7	465	2 S34929	probable membrane
72	73.5	6.7	488	2 T16402	hypothetical prote
73	73.5	6.7	599	2 T16774	hypothetical prote
74	73.5	6.7	624	2 D96494	protein P7F22.10 l
75	73.5	6.7	630	2 A39344	tumor-associated m
76	73.5	6.7	783	2 T30413	vital enhancing fa
77	73.5	6.7	796	2 I48277	cadherin-11 - mous
78	73.5	6.7	796	2 A53584	OB-cadherin precu
79	73.5	6.7	1166	2 H71609	hypothetical prote
80	73	6.6	304	2 A63035	hypothetical prote
81	73	6.6	304	2 D98250	probable sugar ABC
82	73	6.6	315	2 T46993	hypothetical prote
83	73	6.6	381	2 S35940	class I histocompa
84	73	6.6	512	2 C64202	methionine-tRNA 11
85	73	6.6	1181	2 A33998	integrin alpha-2 c
86	73	6.6	2344	2 S55399	genome polypeptid
87	72.5	6.6	231	2 T32953	hypothetical prote
88	72.5	6.6	299	2 I46690	CD80 precursor - r
89	72.5	6.6	682	2 T47473	receptor-like prot
90	72.5	6.6	2829	2 A42771	reticulocyte-bind1
91	72	6.5	283	1 FCM5G1	Fc gamma (IlgG) rec
92	72	6.5	485	2 AG2531	hypothetical prote
93	72	6.5	543	2 T32109	hypothetical prote
94	72	6.5	1036	2 H64245	hypothetical prote
95	72	6.5	1106	2 S38783	integrin alpha cha
96	72	6.5	1447	2 T15200	hypothetical prote
97	72	6.5	5005	2 F82884	hypothetical prote
98	71.5	6.5	331	2 AC1256	E. coli LytB prote
99	71.5	6.5	453	2 C71518	probable permease
100	71.5	6.5	489	2 B53153	glucose transport
101	71.5	6.5	692	2 T05111	hypothetical prote
102	71.5	6.5	796	2 A38992	cadherin 11 precu

hypothetical prote  
protein-tyrosine-p  
ABC transporter At  
tweety protein - F  
G protein-coupled  
probable membrane  
B-cadherin precurs  
Na+/K+-exchanging  
CD44 antigen precu  
lipopolysaccharide  
sensor histidine k  
protein-tyrosine-p  
UDP-N-acetylglucos  
O-antigen transpor  
probable membrane-  
integrin alpha v c  
hypothetical prote  
hypothetical prote  
hypothetical prote  
amino acid permeas  
conserved hypochet  
hypothetical prote  
hypothetical prote  
genome polypeptid  
hypothetical prote  
mucin 1 precursor,  
hypothetical prote  
probable Na+/H+ ex  
hypothetical prote  
mucin 1 precursor,  
glutamate receptor  
glutamate receptor  
hypothetical prote  
hypothetical prote  
episialin - mouse  
receptor-like prot  
hypothetical prote  
opsin, red-sensiti  
glucan 1,4-alpha-m  
B. subtilis yqno p  
probable membrane  
hypothetical prote  
hypothetical prote  
protein P7F22.10 l  
tumor-associated m  
vital enhancing fa  
cadherin-11 - mous  
OB-cadherin precu  
hypothetical prote  
hypothetical prote  
probable sugar ABC  
hypothetical prote  
class I histocompa  
methionine-tRNA 11  
integrin alpha-2 c  
genome polypeptid  
hypothetical prote  
CD80 precursor - r  
receptor-like prot  
reticulocyte-bind1  
Fc gamma (IlgG) rec  
hypothetical prote  
hypothetical prote  
integrin alpha cha  
hypothetical prote  
hypothetical prote  
E. coli LytB prote  
probable permease  
glucose transport  
hypothetical prote  
cadherin 11 precu

103	71.5	6.5	879	2	T02728	serine/threonine-s
104	71.5	6.5	936	2	B64567	cytochrome c bioge
105	71.5	6.5	1038	2	AS2187	hypothetical prote
106	71.5	6.5	1139	2	S28277	hypothetical prote
107	71	6.4	1262	2	T27848	hypothetical prote
108	71	6.4	321	2	AE1606	B. subtilis ynfQ p
109	71	6.4	326	2	S54042	hypothetical prote
110	71	6.4	361	2	JH0417	cell adhesion mole
111	71	6.4	366	2	S53898	probable membrane
112	71	6.4	366	2	AS3286	cell-surface glyco
113	71	6.4	395	2	T77371	CD44S - human
114	71	6.4	489	2	A11276	multidrug-efflux t
115	71	6.4	489	2	A11639	CD44E protein, epi
116	71	6.4	493	2	S13530	hypothetical prote
117	71	6.4	533	2	A72593	hypothetical prote
118	71	6.4	560	2	T18065	gene NMB protein -
119	71	6.4	627	2	H84693	probable protein k
120	71	6.4	685	2	T46843	H+/K+-exchanging A
121	71	6.4	685	2	G97351	K+-transporting AT
122	71	6.4	699	2	I37369	epican - human
123	71	6.4	742	2	A47195	lymphocyte homing
124	71	6.4	826	2	G97073	uncharacterized pr
125	71	6.4	1037	2	AE0163	glycoprotein IIb -
126	71	6.4	1262	2	S68700	Hppp beta-like tyr
127	71	6.4	1268	1	B48758	protein-tyrosine-p
128	71	6.4	1496	1	A48758	protein-tyrosine-p
129	71	6.4	1501	2	T58148	protein-tyrosine-p
130	71	6.4	1863	2	S46237	protein-tyrosine-p
131	71	6.4	1907	2	S50893	genome polyploid
132	71	6.4	2344	1	KRWRH	hypothetical prote
133	71	6.4	5138	2	B96695	alpha-7A integrin
134	70.5	6.4	129	2	I61187	cytochrome P450 83
135	70.5	6.4	516	2	T05940	hypothetical prote
136	70.5	6.4	584	2	T25059	hypothetical prote
137	70.5	6.4	900	2	T04839	protein kinase hom
138	70.5	6.4	1018	2	T19693	hypothetical prote
139	70.5	6.4	1027	1	PMCCNM	Na+/K+-exchanging
140	70.5	6.4	1139	2	T33275	hypothetical prote
141	70.5	6.4	1173	2	S48877	Ca2+-transporting
142	70.5	6.4	2672	2	A48126	translational activa
143	70	6.4	264	2	E72642	hypothetical prote
144	70	6.4	310	2	I64091	cell division prot
145	70	6.4	333	2	D88970	protein F15E11.11
146	70	6.4	362	2	A38545	hypothetical prote
147	70	6.4	402	2	A40678	T-cell adhesion re
148	70	6.4	489	1	RCBVP4	PER494 protein pre
149	70	6.4	544	2	H86828	fructuronate reduc
150	70	6.4	1039	2	A34269	integrin alpha-2b
151	70	6.4	1178	2	S44142	VLA-2 protein homo
152	70	6.4	1635	2	T32452	hypothetical prote
153	70	6.4	1636	2	S60403	probable membrane
154	70	6.4	1721	2	T21214	hypothetical prote
155	69.5	6.3	267	2	B84491	probable replicati
156	69.5	6.3	292	2	CS5147	118B protein limpo
157	69.5	6.3	296	2	A98015	hypothetical prote
158	69.5	6.3	315	2	G98153	peptide ABC transp
159	69.5	6.3	315	2	AE3134	hypothetical prote
160	69.5	6.3	446	2	T45525	MG4 homolog limpo
161	69.5	6.3	479	2	A98232	fructose-like PRS
162	69.5	6.3	481	2	H86078	PRS system, fructo
163	69.5	6.3	523	2	T05994	protein kinase hom
164	69.5	6.3	708	2	T43109	cytolysin B transp
165	69.5	6.3	900	2	T41607	probable vacuolar
166	69.5	6.3	900	2	T33482	hypothetical prote
167	69.5	6.3	1036	2	A42895	H+/K+-exchanging A
168	69.5	6.3	1072	2	T00041	BH-procadinherin P
169	69.5	6.3	1200	2	T00042	BH-procadinherin P
170	69	6.3	231	2	B83031	conserved hypotet
171	69	6.3	369	2	S33250	red visual pigment
172	69	6.3	391	2	H82175	multidrug resistanc
173	69	6.3	616	1	VXZRNA	beta-1,2-glucan ex
174	69	6.3	728	1	A86453	CDS protein PgLI1.
175	69	6.3	773	2	F90537	lipoprotein limpor
176	69	6.3	996	2	T18717	hypothetical prote
177	69	6.3	1017	2	A37227	Na+/K+-exchanging
178	69	6.3	1137	2	JC5950	integrin alpha-7 c
179	69	6.3	1408	2	T45039	hypothetical prote
180	68.5	6.2	141	2	T29781	hypothetical prote
181	68.5	6.2	275	2	T16312	hypothetical prote
182	68.5	6.2	330	2	S08500	QUTG protein - Eme
183	68.5	6.2	342	2	S33355	class I histocoma
184	68.5	6.2	348	2	D82252	Rfd-related prote
185	68.5	6.2	359	2	S20606	3-isopropylmalate
186	68.5	6.2	417	2	C64614	conserved hypotet
187	68.5	6.2	469	2	T34173	hypothetical prote
188	68.5	6.2	481	1	VGXPRV	surface glycoprote
189	68.5	6.2	485	2	A40843	phosphotransferase
190	68.5	6.2	511	2	AE2078	ferrichrome-iron r
191	68.5	6.2	564	2	E70394	ABC transporter (h
192	68.5	6.2	604	2	T36917	glycoprotein IIb -
193	68.5	6.2	796	2	I49556	cadherin-11 - mous
194	68.5	6.2	807	2	T24110	hypothetical prote
195	68.5	6.2	1025	2	S50293	probable membrane
196	68.5	6.2	1101	2	S51823	myosin heavy chain
197	68.5	6.2	1179	2	A53213	integrin alpha-E c
198	68.5	6.2	1192	2	A88925	protein F35E11.3 l
199	68	6.2	168	2	T31451	benzodiazepine rec
200	68	6.2	171	2	T41924	hypothetical prote
201	68	6.2	254	2	T18282	hypothetical prote
202	68	6.2	267	2	A12794	conserved hypotet
203	68	6.2	297	2	E96002	probable sugar upt
204	68	6.2	310	2	H97573	hypothetical prote
205	68	6.2	318	2	H69959	hypothetical prote
206	68	6.2	342	2	AD3450	proline racemase (
207	68	6.2	362	2	A37783	iodopsin - chicken
208	68	6.2	399	2	AB0670	probable virulence
209	68	6.2	429	2	T29711	hypothetical prote
210	68	6.2	529	2	T22398	hypothetical prote
211	68	6.2	538	2	F90604	hypothetical prote
212	68	6.2	542	2	T19862	hypothetical prote
213	68	6.2	544	2	A28671	allantoate transp
214	68	6.2	543	2	T32568	hypothetical prote
215	68	6.2	664	2	T10240	hypothetical prote
216	68	6.2	666	2	T10567	probable serine/th
217	68	6.2	691	2	D84889	probable receptor-
218	68	6.2	878	2	AH2075	ferrichrome-iron x
219	68	6.2	905	1	1JXLC1	N-cadherin 1 precu
220	68	6.2	905	2	A43064	cadherin - African
221	68	6.2	973	2	AH2762	ABC excinuclease s
222	68	6.2	982	2	G97543	exinuclease ABC c
223	68	6.2	1360	2	T31674	hypothetical prote
224	68	6.2	2321	2	S78549	notch protein - h
225	67.5	6.1	207	2	AC3381	hypothetical prote
226	67.5	6.1	270	1	S10532	interleukin-1 alph
227	67.5	6.1	318	2	A49266	fas ligand - rat
228	67.5	6.1	328	2	H71948	probable tetracycl
229	67.5	6.1	330	2	C58931	NMDH2 dehydrogenas
230	67.5	6.1	378	2	T24324	hypothetical prote
231	67.5	6.1	385	2	G70435	hypothetical prote
232	67.5	6.1	387	2	T15462	hypothetical prote
233	67.5	6.1	423	2	H75058	hypothetical prote
234	67.5	6.1	447	2	F82862	conjugal transp
235	67.5	6.1	468	2	H75503	maltoase ABC transp
236	67.5	6.1	489	2	C87480	conserved hypotet
237	67.5	6.1	497	2	A86146	hypothetical prote
238	67.5	6.1	589	2	F97735	hypothetical prote
239	67.5	6.1	608	2	H64473	hypothetical prote
240	67.5	6.1	612	2	B42755	E-selectin precurs
241	67.5	6.1	790	2	T51668	F-cadherin - Afric
242	67.5	6.1	1053	2	S44250	integrin alpha-5 c
243	67.5	6.1	1375	2	T13822	franzied gene prot
244	67.5	6.1	1526	2	T13823	franzied gene prot
245	67.5	6.1	1912	2	A56178	protein-tyrosine-p
246	67	6.1	220	1	RWHU28	T-cell surface gly
247	67	6.1	304	2	T22921	hypothetical prote
248	67	6.1	309	2	E71170	hypothetical prote

249	67	6.1	350	2	JN0621	G protein-coupled	322	66	6.0	956	2	JH0826	glutamate ionotropic
250	67	6.1	364	1	OOHTR	opsin, red-sensiti	323	66	6.0	1115	2	T09433	integrin alpha cha
251	67	6.1	366	1	B95900	DNA polymerase III	324	66	6.0	1115	2	T09403	integrin alpha cha
252	67	6.1	413	1	IKC5A	colicin V secretio	325	66	6.0	1536	1	R8BYS3	regulatory protein
253	67	6.1	467	2	AB0279	probable virulence	326	66	6.0	2089	2	C85426	ATM-like protein I
254	67	6.1	477	2	E98024	hypothetical prote	327	66	6.0	2160	2	T20241	hypothetical prote
255	67	6.1	479	2	C90128	hypothetical prote	328	66	6.0	3738	2	T05501	hypothetical prote
256	67	6.1	506	2	H64618	sigma-54 interacti	329	65.5	5.9	149	2	S73351	adhesin pI homolog
257	67	6.1	506	2	T28930	hypothetical prote	330	65.5	5.9	215	2	A48463	Ras-like GTP-bindi
258	67	6.1	614	2	T28930	hypothetical prote	331	65.5	5.9	220	2	AH3231	conjugal transfer
259	67	6.1	650	2	B84526	hypothetical prote	332	65.5	5.9	231	2	JN0085	hypoxanthine phosph
260	67	6.1	705	2	T31261	hypothetical prote	333	65.5	5.9	271	2	H86166	hypoxanthine phosph
261	67	6.1	717	2	T29816	hypothetical prote	334	65.5	5.9	285	2	S36903	Fe gamma (Igf) rec
262	67	6.1	748	2	A45243	envelope protein H	335	65.5	5.9	331	2	T21156	hypothetical prote
263	67	6.1	782	2	T43277	host cell factor 1	336	65.5	5.9	346	2	T24516	hypothetical prote
264	67	6.1	906	1	TXL1C2	N-cadherin 2 precu	337	65.5	5.9	363	2	A50516	3-isopropylmalate
265	67	6.1	956	2	US0685	glutamate receptor	338	65.5	5.9	413	2	T32831	hypothetical prote
266	67	6.1	1023	1	S24650	Na+/K+-exchanging	339	65.5	5.9	417	2	JC4547	polysaccharide syn
267	67	6.1	1361	2	S50943	hypothetical prote	340	65.5	5.9	435	2	T25350	hypothetical prote
268	66.5	6.0	135	2	F83872	hyaluronan synthas	341	65.5	5.9	450	2	T01711	probable serine/th
269	66.5	6.0	231	2	S06315	hypoxanthine phosph	342	65.5	5.9	476	2	S64425	hypothetical prote
270	66.5	6.0	364	2	I46604	MHC pD14 transplan	343	65.5	5.9	482	1	V6XPT7	surface glycoprote
271	66.5	6.0	366	2	A60369	MHC class I histoc	344	65.5	5.9	485	2	T04840	hypothetical prote
272	66.5	6.0	366	2	I46603	MHC pD14a transpla	345	65.5	5.9	521	2	A99100	phosphatidylinosit
273	66.5	6.0	395	2	A48755	hyaluronan synthas	346	65.5	5.9	543	2	B64232	transport system p
274	66.5	6.0	398	2	I49443	gene 284 protein -	347	65.5	5.9	556	2	S51892	probable membrane
275	66.5	6.0	425	2	A53100	hyaluronate synth	348	65.5	5.9	633	2	S62057	proline-rich prote
276	66.5	6.0	482	2	T28617	hypothetical prote	349	65.5	5.9	644	2	C81187	ABC transporter, A
277	66.5	6.0	489	2	H91174	UDP-MurNac-ctipept	350	65.5	5.9	649	2	C81916	probable ABC trans
278	66.5	6.0	489	2	H86020	probable transport	351	65.5	5.9	709	2	S51793	disaccharide process
279	66.5	6.0	489	2	H86020	probable transport	352	65.5	5.9	817	2	S53921	hypothetical prote
280	66.5	6.0	510	2	C65147	hypothetical 53.7	353	65.5	5.9	895	1	TXL1CP	EP-cadherin precu
281	66.5	6.0	779	2	F84606	probable cytochrom	354	65.5	5.9	906	1	V6BEC1	glycoprotein B pre
282	66.5	6.0	810	2	T31732	hypothetical prote	355	65.5	5.9	921	2	G71705	alkaline phosphata
283	66.5	6.0	830	2	S25198	hypothetical prote	356	65.5	5.9	936	2	H71862	probable cytochrom
284	66.5	6.0	1030	2	T18669	vacuolar membrane	357	65.5	5.9	1011	1	A45598	H+-exporting ATPas
285	66.5	6.0	1081	2	T18669	hypothetical prote	358	65.5	5.9	1049	2	A27079	Fibronectin recept
286	66.5	6.0	1136	2	T26953	receptor tyrosine	359	65.5	5.9	1056	2	T33167	hypothetical prote
287	66.5	6.0	1349	2	A11476	cell surface prote	360	65.5	5.9	1106	1	PRHUB	platelet-derived g
288	66.5	6.0	1371	2	T29019	hypothetical prote	361	65.5	5.9	1113	2	T6954	hypothetical prote
289	66.5	6.0	1371	2	T29019	hypothetical prote	362	65.5	5.9	1348	2	AH1115	cell surface prote
290	66.5	6.0	1770	2	S56221	hypothetical prote	363	65.5	5.9	1356	2	F84486	probable retroelem
291	66	6.0	36	2	C45875	M1 class I histoco	364	65.5	5.9	1387	2	T16511	hypothetical prote
292	66	6.0	179	2	E88028	protein P46Fs.16 I	365	65.5	5.9	1738	2	C84507	hypothetical prote
293	66	6.0	193	2	S73713	Mg319 homolog H08	366	65.5	5.9	108	2	B71074	hypothetical prote
294	66	6.0	226	2	T39298	hypothetical prote	367	65.5	5.9	199	2	A89774	superoxide dismuta
295	66	6.0	250	2	I46850	TL antigen - mouse	368	65.5	5.9	248	1	QQBE4L	probable glycoprot
296	66	6.0	252	2	G90513	hypothetical prote	369	65.5	5.9	249	2	S78186	H+-transporting tw
297	66	6.0	260	2	T27266	hypothetical prote	370	65.5	5.9	262	2	S56524	probable transcrip
298	66	6.0	267	2	B69461	hypothetical prote	371	65.5	5.9	295	2	A99489	arabinose ABC tran
299	66	6.0	284	2	B81421	conserved hypocher	372	65.5	5.9	330	2	A40071	Fe gamma (Igf) rec
300	66	6.0	311	2	T27203	hypothetical prote	373	65.5	5.9	330	2	I49660	Fe-gamma-1/gamma-2
301	66	6.0	357	2	A97384	hypothetical prote	374	65.5	5.9	357	2	T34012	hypothetical prote
302	66	6.0	358	2	A37440	red-sensitive visu	375	65.5	5.9	445	2	H83272	sodium-translocati
303	66	6.0	413	2	T22584	hypothetical prote	376	65.5	5.9	467	2	T16319	hypothetical prote
304	66	6.0	413	2	AD1068	probable sugar tra	377	65.5	5.9	478	2	T21144	hypothetical prote
305	66	6.0	477	2	E95158	hypothetical prote	378	65.5	5.9	482	1	C72254	glycerol kinase -
306	66	6.0	480	2	T04849	protein kinase hom	379	65.5	5.9	483	1	V6XPT5	surface glycoprote
307	66	6.0	503	1	QOKPGP	surface glycoprote	380	65.5	5.9	483	1	V6XPTV	surface glycoprote
308	66	6.0	509	2	T06300	hypothetical prote	381	65.5	5.9	507	2	JC7883	cytochrome P450 4X
309	66	6.0	526	1	A33164	bilary glycoprote	382	65.5	5.9	523	2	T49314	receptor lectin ki
310	66	6.0	539	2	D96562	unknown protein [i	383	65.5	5.9	611	2	T20501	hypothetical prote
311	66	6.0	545	2	T27614	hypothetical prote	384	65.5	5.9	630	1	BMBY	CBP2 protein - yea
312	66	6.0	572	2	T08509	trid. protein - Ent	385	65.5	5.9	637	2	JH0674	L-proline transpor
313	66	6.0	623	2	D71435	hypothetical prote	386	65.5	5.9	661	2	T39114	solute symporter f
314	66	6.0	631	2	JC6031	scaffoldin dockeri	387	65.5	5.9	673	2	S06048	poly(9)glycerol-phos
315	66	6.0	654	2	E64245	periplasmic phosph	388	65.5	5.9	694	2	A13022	potassium-transpor
316	66	6.0	698	1	S31630	NAD+-protein ADP-r	389	65.5	5.9	718	2	A98262	H+/K+-exchanging A
317	66	6.0	705	2	T34521	hypothetical prote	390	65.5	5.9	737	2	T18365	hypothetical prote
318	66	6.0	710	2	T10654	hypothetical prote	391	65.5	5.9	745	2	T18366	anthranilate phosph
319	66	6.0	735	2	T10650	probable receptor-	392	65.5	5.9	748	2	S01659	integrin beta-1 ch
320	66	6.0	782	2	H90742	hypothetical prote	393	65.5	5.9	799	1	IUMSPB	fibronectin recept
321	66	6.0	782	2	C85593	hypothetical prote	394	65.5	5.9	803	2	G96523	FLA17.8 [imported

395	65	5.9	855	2	S42621	protein-tyrosine k		
396	65	5.9	1021	2	A28199	Na+/K+-exchanging		
397	65	5.9	1023	2	A24414	Na+/K+-exchanging		
398	65	5.9	1133	1	EGRT	epidermal growth f		
399	65	5.9	1217	2	T22672	hypothetical prote		
400	65	5.9	1365	2	T45031	hypothetical prote		
401	65	5.9	1720	2	T07258	cell division prot		
402	65	5.9	2809	2	T30213	G-cadherin - sea u		
403	64.5	5.9	148	2	S40148	integrin alpha-7A		
404	64.5	5.9	231	2	S06601	hypoxanthine phosph		
405	64.5	5.9	232	2	H96688	hypothetical prote		
406	64.5	5.9	240	2	H84497	probable replicati		
407	64.5	5.9	270	2	I46620	interleukin-1 alph		
408	64.5	5.9	314	1	B69954	penicillin toleran		
409	64.5	5.9	344	1	I54445	MHC H2-Qa-Mb1 - mo		
410	64.5	5.9	355	2	T14086	hypothetical prote		
411	64.5	5.9	361	2	D53737	phosphate carrier		
412	64.5	5.9	362	2	JH0290	class I histocompa		
413	64.5	5.9	362	2	C53737	phosphate carrier		
414	64.5	5.9	362	2	JQ2037	hypothetical 41K p		
415	64.5	5.9	378	2	S00842	leukostallin precu		
416	64.5	5.9	403	2	G83272	sodium-translocati		
417	64.5	5.9	416	2	A82095	conserved hypotnet		
418	64.5	5.9	420	2	C64552	exonuclease VII, 1		
419	64.5	5.9	426	2	T45767	hypothetical prote		
420	64.5	5.9	427	2	S44549	probable membrane		
421	64.5	5.9	462	2	B57145	histidine kinase p		
422	64.5	5.9	464	2	C30127	transmembrane carc		
423	64.5	5.9	474	2	T01004	hypothetical prote		
424	64.5	5.9	505	2	T28859	inward rectifier p		
425	64.5	5.9	571	2	B89800	conserved hypotnet		
426	64.5	5.9	585	2	G86200	protein F12K11.15		
427	64.5	5.9	662	2	S61193	probable membrane		
428	64.5	5.9	700	2	T49445	adenoleukodystrop		
429	64.5	5.9	703	2	T24975	hypothetical prote		
430	64.5	5.9	790	2	T50178	cadherin-6B - chic		
431	64.5	5.9	826	2	C96694	hypothetical prote		
432	64.5	5.9	859	1	VCLJST	env polypeptid pr		
433	64.5	5.9	877	1	IJB0CN	N-cadherin precurs		
434	64.5	5.9	906	1	IJHUCN	cadherin 2 precurs		
435	64.5	5.9	906	1	IJMSCN	N-cadherin precurs		
436	64.5	5.9	912	1	IJCHCN	N-cadherin precurs		
437	64.5	5.9	913	1	IJCHCR	R-cadherin precurs		
438	64.5	5.9	979	2	JH0589	glutamate receptor		
439	64.5	5.9	979	2	JH0592	glutamate receptor		
440	64.5	5.9	1036	2	T38734	hypothetical prote		
441	64.5	5.9	1075	2	D70568	hypothetical prote		
442	64.5	5.9	1338	2	T18287	hypothetical prote		
443	64.5	5.9	1346	2	T17412	protein-tyrosine k		
444	64	5.8	108	2	S40149	integrin alpha-7C		
445	64	5.8	216	2	D70655	probable regulator		
446	64	5.8	249	2	T16228	hypothetical prote		
447	64	5.8	255	2	AD1159	flagellar biosynth		
448	64	5.8	283	2	F88087	protein B0454.5 [i		
449	64	5.8	285	2	H95943	probable sugar upt		
450	64	5.8	288	2	B45897	MHC class I histoc		
451	64	5.8	315	2	T37438	hemagglutinin - va		
452	64	5.8	329	2	T23115	hypothetical prote		
453	64	5.8	343	2	T03128	hypothetical prote		
454	64	5.8	343	2	A11143	hypothetical prote		
455	64	5.8	372	2	S67770	probable membrane		
456	64	5.8	380	2	S34964	ric protein - Shlg		
457	64	5.8	389	2	S22839	translaton activa		
458	64	5.8	415	2	A35560	lysosomal membrane		
459	64	5.8	421	2	D97078	MOR-type permease		
460	64	5.8	441	2	C86378	protein F2139.6 [i		
461	64	5.8	443	2	F85972	probable transport		
462	64	5.8	443	2	G91127	probable transport		
463	64	5.8	457	2	F83064	probable MFS trans		
464	64	5.8	462	2	T04437	hypothetical prote		
465	64	5.8	506	2	F71895	hypothetical prote		
466	64	5.8	522	2	A31556	glucose transport		
467	64	5.8	543	2	F84861	hypothetical prote		
468	64	5.8	468	64	575	2	S46692	hypothetical prote
469	64	5.8	469	64	695	1	WHIMV	nucleoscapid prote
470	64	5.8	470	64	716	2	T21516	hypothetical prote
471	64	5.8	471	64	754	2	A85043	probable LRR recep
472	64	5.8	472	64	769	2	F89870	serine proteinase
473	64	5.8	473	64	799	2	UC4126	integrin beta olig
474	64	5.8	474	64	819	2	A84504	lipoxygenase (EC 1
475	64	5.8	475	64	862	2	T05941	Mutator-like trans
476	64	5.8	476	64	865	2	C86639	preproteain translo
477	64	5.8	477	64	880	2	G90163	DNA-directed RNA p
478	64	5.8	478	64	880	2	H82883	hypothetical prote
479	64	5.8	479	64	1003	1	S00801	Na+/K+-exchanging
480	64	5.8	480	64	1013	2	C24639	Na+/K+-exchanging
481	64	5.8	481	64	1020	2	A34474	Na+/K+-exchanging
482	64	5.8	482	64	1021	2	B24862	Na+/K+-exchanging
483	64	5.8	483	64	1022	1	S00503	Na+/K+-exchanging
484	64	5.8	484	64	1023	1	A24639	Na+/K+-exchanging
485	64	5.8	485	64	1070	2	E71401	probable selenium-
486	64	5.8	486	64	1168	2	T37496	probable pre-mRNA
487	64	5.8	487	64	1265	2	T21782	hypothetical prote
488	64	5.8	488	64	1398	2	T21884	hypothetical prote
489	64	5.8	489	64	1556	2	F96587	hypothetical prote
490	64	5.8	490	64	1898	2	S46216	leukocyte antigen-
491	64	5.8	491	64	2167	2	AF1489	cell wall-associat
492	64	5.8	492	64	2655	2	D96595	probable acetyl-Co
493	64	5.8	493	64	3890	2	C89921	hypothetical prote
494	63.5	5.8	494	63.5	117	2	G75135	hypothetical prote
495	63.5	5.8	495	63.5	192	2	A40606	superinfection exc
496	63.5	5.8	496	63.5	216	2	T76676	gene Ran protein -
497	63.5	5.8	497	63.5	244	2	AD1225	cobalamin biosynth
498	63.5	5.8	498	63.5	244	2	AF1578	hypothetical prote
499	63.5	5.8	499	63.5	244	2	G96507	hypothetical prote
500	63.5	5.8	500	63.5	247	2	S53863	H+-transporting tw
501	63.5	5.8	501	63.5	272	1	UHHU2	interleukin-2 rece
502	63.5	5.8	502	63.5	297	2	G87187	phosphoribosylam
503	63.5	5.8	503	63.5	338	2	JC5435	aspartate-semialde
504	63.5	5.8	504	63.5	338	2	UC5436	aspartate-semialde
505	63.5	5.8	505	63.5	362	1	QQBED2	HNRF2 protein - hu
506	63.5	5.8	506	63.5	364	2	B85430	hypothetical prote
507	63.5	5.8	507	63.5	386	2	T39588	hypothetical prote
508	63.5	5.8	508	63.5	395	2	I52842	CD43 lp-3 antigen
509	63.5	5.8	509	63.5	395	2	A43545	leukostallin CD43
510	63.5	5.8	510	63.5	423	2	A64466	dihydroorotase (EC
511	63.5	5.8	511	63.5	425	2	C65100	hypothetical 46.6
512	63.5	5.8	512	63.5	466	2	T32204	hypothetical prote
513	63.5	5.8	513	63.5	476	2	AF0191	probable sugar tra
514	63.5	5.8	514	63.5	492	1	C69762	di-tripeptide ABC
515	63.5	5.8	515	63.5	501	2	A86781	membrane-bound tra
516	63.5	5.8	516	63.5	508	2	A33378	fasciclin III prec
517	63.5	5.8	517	63.5	514	2	T29652	inward rectifier p
518	63.5	5.8	518	63.5	525	2	S49650	probable membrane
519	63.5	5.8	519	63.5	533	2	T46975	lysine-tRNA ligase
520	63.5	5.8	520	63.5	559	2	AF0891	probable exported
521	63.5	5.8	521	63.5	573	2	AB2401	hypothetical prote
522	63.5	5.8	522	63.5	605	2	G69060	threonine-tRNA lig
523	63.5	5.8	523	63.5	663	1	S30051	arachidonate 12-11
524	63.5	5.8	524	63.5	707	2	T30712	probable early tra
525	63.5	5.8	525	63.5	732	1	JU0132	acylaminoacyl-pept
526	63.5	5.8	526	63.5	820	2	A86510	leucyl tRNA synthe
527	63.5	5.8	527	63.5	820	2	C72113	leucine-tRNA ligas
528	63.5	5.8	528	63.5	830	2	T07824	1,4-alpha-glucan b
529	63.5	5.8	529	63.5	833	2	AB0448	probable inaectici
530	63.5	5.8	530	63.5	863	2	C90482	ABC transporter, A
531	63.5	5.8	531	63.5	913	1	A47543	R-cadherin precurs
532	63.5	5.8	532	63.5	921	2	G02336	transcription fact
533	63.5	5.8	533	63.5	978	2	T16948	hypothetical prote
534	63.5	5.8	534	63.5	980	2	I57936	glutamate receptor
535	63.5	5.8	535	63.5	1051	2	A35761	cell surface glyco
536	63.5	5.8	536	63.5	1428	2	C85079	hypothetical prote
537	63.5	5.8	537	63.5	1628	2	T43682	nucleoporin - fms
538	63.5	5.8	538	63.5	1691	1	D54689	protein-tyrosine-p
539	63.5	5.8	539	63.5	1894	2	C54689	protein-tyrosine-p
540	63.5	5.8	540	63.5	2403	2	T30875	pp88 protein homol



541	63	5.7	98	2	T17086	NADH2 dehydrogenas	614	62.5	5.7	449	2	H88545	protein F59B2.13 [
542	63	5.7	229	2	E95265	probable GntR-fam1	615	62.5	5.7	451	2	T40736	probable pseudouri
543	63	5.7	253	2	T19129	hypothetical prote	616	62.5	5.7	474	2	T27006	hypothetical prote
544	63	5.7	289	2	C69346	hypothetical prote	617	62.5	5.7	475	2	T24850	hypothetical prote
545	63	5.7	299	2	G90386	conserved hypothet	618	62.5	5.7	480	2	T24422	amidophosphoribosy
546	63	5.7	310	2	G81381	probable integral	619	62.5	5.7	493	1	ACRYB1	nicotinic acetylch
547	63	5.7	315	1	HNW24X	hemagglutinin prec	620	62.5	5.7	496	2	T52112	deoxyribodipyrimid
548	63	5.7	315	1	HNWZVT	hemagglutinin prec	621	62.5	5.7	508	2	T41345	probable allantoad
549	63	5.7	330	2	A22915	teratocarcinoma gl	622	62.5	5.7	519	2	S31133	hypothetical prote
550	63	5.7	334	2	T11633	hypothetical prote	623	62.5	5.7	531	2	T18931	hypothetical prote
551	63	5.7	354	2	T09353	G protein-coupled	624	62.5	5.7	538	2	B56636	retinoid element PA
552	63	5.7	359	2	S24240	lymphocyte surfac	625	62.5	5.7	596	2	AC1318	two-component sens
553	63	5.7	361	2	T31815	hypothetical prote	626	62.5	5.7	635	2	S36718	phosphoprotein pho
554	63	5.7	370	2	A30901	lymphocyte adhesio	627	62.5	5.7	645	2	E96631	probable receptor
555	63	5.7	372	1	B35255	chloromucronate cyc	628	62.5	5.7	672	2	D96006	probable cytochrom
556	63	5.7	396	2	H69817	aminoacylase homol	629	62.5	5.7	679	2	A56765	sodium-glucose cot
557	63	5.7	411	2	A33664	96K lysosomal memb	630	62.5	5.7	695	2	G64327	H+-transporting tw
558	63	5.7	452	2	D64961	membrane protein Y	631	62.5	5.7	705	2	S70029	probable transmemb
559	63	5.7	457	2	S13872	nicotinic acetylch	632	62.5	5.7	721	2	JC7557	lipidosis - mouse
560	63	5.7	468	2	D84503	probable serine ca	633	62.5	5.7	776	2	C96554	unknown protein [i
561	63	5.7	497	2	G97738	histidine kinase s	634	62.5	5.7	785	2	I50180	cadherin-7 - chick
562	63	5.7	498	2	A10482	phosphate transpor	635	62.5	5.7	789	2	I52701	K-cadherin - rat
563	63	5.7	499	2	E91174	low-affinity phosph	636	62.5	5.7	790	2	I37016	cadherin-6 - human
564	63	5.7	499	2	E86020	plc $\alpha$ protein - Eac	637	62.5	5.7	802	2	B43735	bcsb protein - Ace
565	63	5.7	499	2	S47713	zinc transporter Z	638	62.5	5.7	809	2	AS7283	integrin beta chain
566	63	5.7	503	2	S54302	iron (III) transpo	639	62.5	5.7	888	2	S23065	ufo protein - mous
567	63	5.7	553	2	B83714	s-glycerin precurs	640	62.5	5.7	894	1	A41527	protein-tyrosine k
568	63	5.7	584	2	I50419	serum albumin prec	641	62.5	5.7	907	1	VB8ETE	glycoprotein B pre
569	63	5.7	600	2	A47391	nuclear envelope p	642	62.5	5.7	1019	2	T13039	tyrosine kinase re
570	63	5.7	601	2	T47249	hypothetical prote	643	62.5	5.7	1095	2	G96746	hypothetical prote
571	63	5.7	610	2	T33327	hypothetical prote	644	62.5	5.7	1122	2	S64443	probable membrane
572	63	5.7	663	2	T24881	conserved hypothet	645	62.5	5.7	1213	2	T37959	hypothetical prote
573	63	5.7	673	2	P95079	conserved hypothet	646	62.5	5.7	1226	2	E84923	hypothetical prote
574	63	5.7	674	2	A97947	glycoprotein H - h	647	62.5	5.7	1333	2	A37488	Ras guanine nucleo
575	63	5.7	693	2	JQ2383	NAD+-protein ADP-r	648	62.5	5.7	1391	2	T20642	hypothetical prote
576	63	5.7	728	1	S31714	sodium-dependent n	649	62.5	5.7	1397	2	E87998	protein F09C3.1 [i
577	63	5.7	728	1	I65413	probable membrane	650	62.5	5.7	1592	2	S48933	probable transport
578	63	5.7	730	2	I52632	env polypeptid pr	651	62.5	5.7	1896	2	T08851	Down syndrome cell
579	63	5.7	782	2	A64821	probable NADH dehy	652	62.5	5.7	2229	2	T16199	hypothetical prote
580	63	5.7	852	1	VCLJGG	probable NADH dehy	653	62.5	5.7	2802	2	F97686	cyclic beta-(1-2)
581	63	5.7	891	2	B82495	Na+/K+-exchanging	654	62.5	5.7	2831	2	A12911	beta (1->2) glucan
582	63	5.7	996	2	JE0237	Na+/K+-exchanging	655	62.5	5.6	57	2	I47032	integrin alpha 5 -
583	63	5.7	996	2	B37227	Na+/K+-exchanging	656	62.5	5.6	100	2	H83987	hypothetical prote
584	63	5.7	1020	2	B24639	Na+/K+-exchanging	657	62.5	5.6	144	2	S67078	probable membrane
585	63	5.7	1021	1	PM8HNA	Na+/K+-exchanging	658	62.5	5.6	255	2	AD1518	flagellar biosynth
586	63	5.7	1021	1	S04630	beta transducin-11	659	62.5	5.6	263	2	T23347	hypothetical prote
587	63	5.7	1049	2	T42045	pre-mRNA splicing	660	62.5	5.6	269	2	P96506	hypothetical prote
588	63	5.7	1226	2	T49915	hepatocyte growth	661	62.5	5.6	277	2	B64548	conserved hypothet
589	63	5.7	1379	1	S01254	position-specific	662	62.5	5.6	289	2	S72554	melatonin receptor
590	63	5.7	1394	2	A29637	hypothetical prote	663	62.5	5.6	290	2	S48301	geranylgeranyl tra
591	63	5.7	1642	2	T19130	SEC7 protein - yea	664	62.5	5.6	310	2	D71878	stress protein - H
592	63	5.7	2009	2	S49764	hypothetical prote	665	62.5	5.6	311	2	E82468	hypothetical prote
593	62.5	5.7	169	2	S76351	thermoresistant gl	666	62.5	5.6	312	2	A10138	probable cation tr
594	62.5	5.7	171	2	F82340	probable transcrip	667	62.5	5.6	318	2	H64687	magnesium and cob
595	62.5	5.7	214	2	H86916	GTP-binding protei	668	62.5	5.6	327	2	P88102	protein W10G11.11
596	62.5	5.7	216	2	S59942	cobalamin biosynth	669	62.5	5.6	327	2	T10263	probable polygalac
597	62.5	5.7	220	2	A84316	probable membrane	670	62.5	5.6	353	2	A38421	opsin, green-sensi
598	62.5	5.7	234	2	G64858	hypothetical prote	671	62.5	5.6	368	2	B93633	hypothetical prote
599	62.5	5.7	277	2	T23186	hypothetical prote	672	62.5	5.6	375	2	T06096	oligosaccharide tran
600	62.5	5.7	278	2	S46057	probable endo-xylo	673	62.5	5.6	376	2	F64208	potassium channel
601	62.5	5.7	279	2	T09870	hypothetical prote	674	62.5	5.6	376	2	S48739	hypothetical prote
602	62.5	5.7	295	2	AB3164	hypothetical prote	675	62.5	5.6	392	2	T29519	hypothetical prote
603	62.5	5.7	305	2	T27151	two-component syst	676	62.5	5.6	394	2	G85829	O antigen polymera
604	62.5	5.7	328	2	E86837	NADH2 dehydrogenas	677	62.5	5.6	425	2	D90984	conserved hypothet
605	62.5	5.7	346	2	T11390	hypothetical prote	678	62.5	5.6	425	2	E36035	thrombin receptor
606	62.5	5.7	351	2	A12325	acid phosphatase (	679	62.5	5.6	433	2	A43448	hypothetical prote
607	62.5	5.7	385	1	JH0610	hypothetical prote	680	62.5	5.6	433	2	T17654	outer membrane pro
608	62.5	5.7	386	1	JH0610	hypothetical prote	681	62.5	5.6	482	2	T27219	hypothetical prote
609	62.5	5.7	398	2	S56369	hypothetical 44.8K	682	62.5	5.6	483	2	B64548	nicotinic acetylch
610	62.5	5.7	418	2	D86003	hypothetical prote	683	62.5	5.6	493	2	S68587	probable membrane
611	62.5	5.7	428	2	P91157	probable membrane	684	62.5	5.6	493	2	T24695	probable phosphate
612	62.5	5.7	428	2	P91157	probable membrane	685	62.5	5.6	493	2	T24695	probable phosphate
613	62.5	5.7	431	2	F90316	probable membrane	686	62.5	5.6	533	2	A71812	probable phosphate

687	62	5.6	560	2	S64091	probable membrane	760	61.5	5.6	531	2	A55788	glucuronosyltransf
688	62	5.6	592	2	B82498	sulfate permease f	761	61.5	5.6	544	2	AE1563	pyruvate dehydroge
689	62	5.6	613	2	JC7762	SOX-3 protein - gu	762	61.5	5.6	568	2	E96648	hypothetical prote
690	62	5.6	651	2	P90536	transport protein	763	61.5	5.6	578	2	H86365	tg6312.7 protein -
691	62	5.6	656	2	A49579	amphotropic mutine	764	61.5	5.6	580	2	B84554	hypothetical prote
692	62	5.6	660	2	S73673	hypothetical prote	765	61.5	5.6	589	2	B41918	probable secretom
693	62	5.6	662	2	G88451	protein K102.6 [1	766	61.5	5.6	592	2	A96523	hypothetical prote
694	62	5.6	669	2	T47484	receptor like prot	767	61.5	5.6	602	2	S60052	calcium-dependent
695	62	5.6	680	2	P95418	probable KdPB pola	768	61.5	5.6	646	2	T28868	hypothetical prote
696	62	5.6	732	1	MXRMW4	nonstructural prot	769	61.5	5.6	663	2	I52462	arachidonate 12-11
697	62	5.6	743	2	A97021	pyruvate-formate l	770	61.5	5.6	665	2	H87468	ubiquinol oxidase
698	62	5.6	778	2	T05341	S-receptor kinase	771	61.5	5.6	675	2	D85065	receptor protein k
699	62	5.6	790	2	G02678	cadherin-14 - huma	772	61.5	5.6	704	2	S25371	DBF4 protein - yea
700	62	5.6	895	2	S20582	aspartate kinase (	773	61.5	5.6	715	2	G86634	hypothetical prote
701	62	5.6	916	2	T04752	probable ligand-ga	774	61.5	5.6	740	2	F82614	conserved hypochet
702	62	5.6	920	2	B84640	receptor-like prot	775	61.5	5.6	783	2	I50116	N-cadherin precurs
703	62	5.6	932	2	T46489	alpha-adaptin C -	776	61.5	5.6	825	1	A60386	interleukin-4 rece
704	62	5.6	938	2	B30111	alpha-adaptin C -	777	61.5	5.6	826	2	G90283	hypothetical prote
705	62	5.6	938	2	S11276	alpha-adaptin c -	778	61.5	5.6	846	2	T21700	hypothetical prote
706	62	5.6	1064	2	T01960	integrin alpha-6 c	779	61.5	5.6	865	2	T41909	probable membrane
707	62	5.6	1073	2	B36429	exodeoxyribonuclea	780	61.5	5.6	936	2	S64384	hypothetical prote
708	62	5.6	1169	2	H70178	two-component hydr	781	61.5	5.6	968	2	T45746	probable membrane
709	62	5.6	1194	2	AE2041	1-phosphatidylinos	782	61.5	5.6	1055	2	C82600	multidrug-efflux t
710	62	5.6	1236	1	A53970	hypothetical prote	783	61.5	5.6	1379	2	S64603	YnfA7 protein - yea
711	62	5.6	1247	2	T45743	xanthine dehydroge	784	61.5	5.6	4969	2	A37113	riyandine receptor
712	62	5.6	1331	1	XORTDH	probable membrane	785	61.5	5.5	71	2	B83730	hypothetical prote
713	62	5.6	1656	2	S54520	probable dehydroge	786	61.5	5.5	109	2	F82628	conserved hypochet
714	62	5.6	1657	2	T19536	hypothetical prote	787	61.5	5.5	110	1	D38530	preproteins translo
715	62	5.6	1692	2	G01449	probable mucin G2	788	61.5	5.5	110	2	AF0552	preproteins translo
716	62	5.6	2062	2	G96602	probable receptor	789	61.5	5.5	110	2	B90686	preproteins translo
717	61.5	5.6	92	2	S03214	hypothetical prote	790	61.5	5.5	110	2	F85356	preproteins translo
718	61.5	5.6	121	2	I46048	MHC class I antige	791	61.5	5.5	166	2	JC1348	hypothetical 18k p
719	61.5	5.6	150	2	T33646	hypothetical prote	792	61.5	5.5	207	2	T12097	GTP-binding protei
720	61.5	5.6	193	2	C91003	probable superinfe	793	61.5	5.5	218	2	A43523	T-cell surface gly
721	61.5	5.6	204	2	H70008	hypothetical prote	794	61.5	5.5	230	2	F83697	ABC transporter (A
722	61.5	5.6	212	1	VQ03B3	BaR protein 3 - B	795	61.5	5.5	245	2	T18606	hypothetical prote
723	61.5	5.6	216	1	TVHUC3	GTP-binding protei	796	61.5	5.5	252	2	A69096	nitrogenase reduct
724	61.5	5.6	216	2	S24031	GTP-binding protei	797	61.5	5.5	263	2	E72675	hypothetical prote
725	61.5	5.6	216	2	JC1455	GTP-binding protei	798	61.5	5.5	273	2	T37841	probable transloca
726	61.5	5.6	216	2	I57020	GTP-binding protei	799	61.5	5.5	273	2	T31892	hypothetical prote
727	61.5	5.6	225	2	T45889	hypothetical prote	800	61.5	5.5	277	2	F71960	hypothetical prote
728	61.5	5.6	284	2	A45840	MHC class I histoc	801	61.5	5.5	278	2	AB3413	signal peptidase I
729	61.5	5.6	291	2	B82258	cell division prot	802	61.5	5.5	288	2	G87319	hypothetical prote
730	61.5	5.6	314	2	T15674	hypothetical prote	803	61.5	5.5	290	2	T22161	hypothetical prote
731	61.5	5.6	318	2	T11260	NMDH2 dehydrogenas	804	61.5	5.5	299	2	T39602	conserved hypochet
732	61.5	5.6	326	2	T43219	serine/threonine-s	805	61.5	5.5	300	2	AE2088	hypothetical prote
733	61.5	5.6	330	2	C95844	probable sugar ABC	806	61.5	5.5	307	2	T39783	hypothetical prote
734	61.5	5.6	334	2	E71103	probable aspartate	807	61.5	5.5	314	2	F83822	penicillin toleran
735	61.5	5.6	339	2	T29405	hypothetical prote	808	61.5	5.5	340	2	G64029	hypothetical prote
736	61.5	5.6	343	2	D89124	protein K07C11.2 [	809	61.5	5.5	350	2	T25366	hypothetical prote
737	61.5	5.6	345	2	S55377	uPAB protein prec	810	61.5	5.5	352	2	AF0692	probable membrane
738	61.5	5.6	356	2	JH0289	class I histocoma	811	61.5	5.5	355	2	H95320	Nodi membrane tran
739	61.5	5.6	368	2	G86427	probable pectate l	812	61.5	5.5	396	2	H84606	hypothetical prote
740	61.5	5.6	393	2	G71173	hypothetical prote	813	61.5	5.5	418	2	E91037	hypothetical prote
741	61.5	5.6	394	2	C96500	hypothetical prote	814	61.5	5.5	418	2	G85881	hypothetical prote
742	61.5	5.6	399	2	AE0549	probable efflux pu	815	61.5	5.5	420	2	B65013	hypothetical prote
743	61.5	5.6	404	2	S34031	KRX3 protein - yea	816	61.5	5.5	428	2	S50864	sugar ABC transpor
744	61.5	5.6	413	2	T44804	type I site-specific	817	61.5	5.5	430	2	C72014	poly A polymerase
745	61.5	5.6	418	2	H86109	probable transport	818	61.5	5.5	433	2	T31511	hypothetical prote
746	61.5	5.6	418	2	B98269	probable transport	819	61.5	5.5	435	2	T19667	hypothetical prote
747	61.5	5.6	425	2	S33045	hypothetical prote	820	61.5	5.5	435	2	S35732	dnax protein - sp1
748	61.5	5.6	428	1	Q4ECAD	damx protein (arob	821	61.5	5.5	450	2	S50864	avermectin-sensiti
749	61.5	5.6	457	2	S47938	amino-terminal ami	822	61.5	5.5	461	2	S42084	basic protein - C1
750	61.5	5.6	471	2	F72257	11p0polysaccharide	823	61.5	5.5	465	2	B55748	protein kinase (EC
751	61.5	5.6	476	2	I80182	activin type I rec	824	61.5	5.5	482	2	G86227	protein kinase (EC
752	61.5	5.6	487	2	I80183	activin type I rec	825	61.5	5.5	499	2	A89015	protein B0213.10 [
753	61.5	5.6	489	2	AD0988	T-complex protein	826	61.5	5.5	501	2	A99319	transporter/Fac11
754	61.5	5.6	502	2	B90103	type I serine-thre	827	61.5	5.5	528	2	S57835	IgG-binding protei
755	61.5	5.6	505	2	I53417	activin A receptor	828	61.5	5.5	531	2	S41986	26S proteasome reg
756	61.5	5.6	505	2	I38859	adp-ATP carrier pr	829	61.5	5.5	532	2	S27372	beta-fructofuranos
757	61.5	5.6	511	1	B97783	beta-globulin B pr	830	61.5	5.5	533	2	C64706	phosphate permease
758	61.5	5.6	516	1	FWCNRB	hypothetical prote	831	61.5	5.5	536	2	H86192	hypothetical prote
759	61.5	5.6	528	2	T21834	hypothetical prote	832	61.5	5.5				

833	61	5.5	574	2	S57072	hypothetical prote
834	61	5.5	579	1	WZBR34	gene 34 protein -
835	61	5.5	632	1	VGWNSY	surface glycoprote
836	61	5.5	681	2	T23811	hypothetical prote
837	61	5.5	689	2	F83843	hypothetical prote
838	61	5.5	712	2	D87418	proton pump, proba
839	61	5.5	721	2	S49789	hypothetical prote
840	61	5.5	749	2	T44796	DNA helicase pcrA
841	61	5.5	798	2	A28193	integrin beta-1 ch
842	61	5.5	822	2	B28193	integrin beta-1* c
843	61	5.5	822	2	S56801	hypothetical prote
844	61	5.5	834	2	JC7993	env protein - huma
845	61	5.5	859	2	S24571	protein kinase (EC
846	61	5.5	895	2	A86410	peptidase, M16 fam
847	61	5.5	926	2	A55748	beta transducin ho
848	61	5.5	976	2	A87576	hypothetical prote
849	61	5.5	981	2	T18234	hypothetical prote
850	61	5.5	993	2	T25624	hypothetical prote
851	61	5.5	1006	2	AD2195	hypothetical prote
852	61	5.5	1012	2	T00958	hypothetical prote
853	61	5.5	1027	2	T38759	zinc finger/leucin
854	61	5.5	1146	2	S40311	integrin - fruit f
855	61	5.5	1273	1	TDR1LT	leukocyte common a
856	61	5.5	1472	2	S67195	probable membrane
857	61	5.5	1564	2	T27121	hypothetical prote
858	61	5.5	1729	2	S57596	ribosomal RNA proc
859	61	5.5	1858	2	T18273	1-phosphatidylinos
860	61	5.5	2051	2	T30938	receptor tyrosine
861	61	5.5	2102	2	T15626	hypothetical prote
862	61	5.5	2352	2	T43431	alpha-glucan synth
863	61	5.5	3944	2	T19997	hypothetical prote
864	60.5	5.5	87	2	E69071	hypothetical prote
865	60.5	5.5	87	2	G64328	hypothetical prote
866	60.5	5.5	152	2	S19388	probable membrane
867	60.5	5.5	172	2	S52801	hypothetical prote
868	60.5	5.5	179	2	H86211	protein P24B9.22 (
869	60.5	5.5	188	2	A34014	integrin alpha-3 c
870	60.5	5.5	196	2	AD2304	hypothetical prote
871	60.5	5.5	203	2	T49054	Ly-49G.2 antigen -
872	60.5	5.5	219	2	AB1115	hypothetical prote
873	60.5	5.5	222	2	A89776	capular polyacch
874	60.5	5.5	259	2	G86962	probable membrane
875	60.5	5.5	259	2	A86822	hypothetical prote
876	60.5	5.5	267	2	T49053	Ly-49G.2 antigen -
877	60.5	5.5	280	2	T49052	Ly-49G.1 antigen -
878	60.5	5.5	305	2	C69609	cytochrome caa3 ox
879	60.5	5.5	323	2	F69454	signal-transducin
880	60.5	5.5	330	2	T29141	hypothetical prote
881	60.5	5.5	333	2	S78136	NADH2 dehydrogenas
882	60.5	5.5	334	2	T36052	probable cytochrom
883	60.5	5.5	340	2	A64902	peptide transport
884	60.5	5.5	343	2	H96703	probable RING zinc
885	60.5	5.5	347	2	G84898	hemian transport sy
886	60.5	5.5	356	2	G82938	class I histocompa
887	60.5	5.5	357	2	S11133	3-isopropylmalate
888	60.5	5.5	358	1	F64106	MHC class I histoc
889	60.5	5.5	361	2	B27638	class I histocompa
890	60.5	5.5	365	2	T56053	oncogene 1 - human
891	60.5	5.5	376	2	S57867	integral membrane
892	60.5	5.5	379	2	A82806	arginine decarboxy
893	60.5	5.5	401	2	T14429	hypothetical prote
894	60.5	5.5	403	2	A83344	NADH2 dehydrogenas
895	60.5	5.5	407	2	S76637	hypothetical prote
896	60.5	5.5	413	2	Af0393	NADH2 dehydrogenas
897	60.5	5.5	418	2	E83686	exodeoxyribonuclea
898	60.5	5.5	420	2	E71955	S-locus-specific g
899	60.5	5.5	429	2	T14524	hypothetical prote
900	60.5	5.5	445	2	T23725	hypothetical prote
901	60.5	5.5	456	2	T24504	hypothetical prote
902	60.5	5.5	457	1	ACHDA1	nicotinic acetylch
903	60.5	5.5	463	2	AE1155	amino acid transpo
904	60.5	5.5	470	2	S39733	amino acid permeas
905	60.5	5.5	479	2	H97773	osmolality sensor
906	60.5	5.5	497	2	T39680	probable allantocat
907	60.5	5.5	501	2	T36051	probable cytochrom
908	60.5	5.5	511	2	G64902	extreme acid resis
909	60.5	5.5	511	2	A90891	acid sensitivity p
910	60.5	5.5	516	2	H85726	acid sensitivity p
911	60.5	5.5	516	2	AB3088	MPS permease (prol
912	60.5	5.5	516	2	G98198	proline/betaine tr
913	60.5	5.5	529	2	S62468	probable membrane
914	60.5	5.5	537	2	T40507	probable vacuolar
915	60.5	5.5	543	2	A53790	cytochrome P450-BF
916	60.5	5.5	544	2	AF1206	pyruvate dehydroge
917	60.5	5.5	546	2	T24679	hypothetical prote
918	60.5	5.5	557	2	T22079	hypothetical prote
919	60.5	5.5	560	2	S27387	interferon alpha r
920	60.5	5.5	563	2	AD1019	probable sodium/hy
921	60.5	5.5	578	2	H82872	hypothetical prote
922	60.5	5.5	589	2	T38232	phenylalanine-tRNA
923	60.5	5.5	611	2	T28171	hypothetical prote
924	60.5	5.5	622	2	AC0952	hypothetical prote
925	60.5	5.5	622	2	T37257	membrane transport
926	60.5	5.5	636	2	UC5874	hypothetical prote
927	60.5	5.5	637	2	T04552	cellulase (EC 3.2.
928	60.5	5.5	662	2	D40228	hypothetical prote
929	60.5	5.5	694	2	H95012	neurexin II-beta p
930	60.5	5.5	702	2	C97884	hypothetical prote
931	60.5	5.5	722	2	F86233	hypothetical prote
932	60.5	5.5	737	2	T33349	hypothetical prote
933	60.5	5.5	751	2	C84367	DNA binding protei
934	60.5	5.5	767	2	B84594	probable LRR recep
935	60.5	5.5	786	2	S22155	oncogene 1 (tre-2
936	60.5	5.5	820	2	AE2130	ferrichrome-iron r
937	60.5	5.5	833	2	T24682	hypothetical prote
938	60.5	5.5	905	2	S66295	SAP155 protein - y
939	60.5	5.5	935	2	S66306	hypothetical prote
940	60.5	5.5	985	1	VCLJSP	env polypeptide -
941	60.5	5.5	1023	2	T31669	neural zinc finger
942	60.5	5.5	1051	2	A40021	integrin alpha-3 c
943	60.5	5.5	1059	2	T00943	BH-protocadherin-a
944	60.5	5.5	1170	2	T55914	integrin alpha 2 b
945	60.5	5.5	1259	2	G86119	hypothetical prote
946	60.5	5.5	1259	2	G91278	hypothetical prote
947	60.5	5.5	1715	2	C40228	neurexin II-alpha
948	60.5	5.5	2195	2	S61103	SECI6 protein - ye
949	60.5	5.5	2285	1	G02434	DNA-directed DNA p
950	60.5	5.5	2500	2	G88493	protein P57B9.2 (i
951	60.5	5.5	3649	1	S18268	delta-(U-alpha-aml
952	60	5.4	108	2	A86794	hypothetical prote
953	60	5.4	136	2	S04576	Ig heavy chain pre
954	60	5.4	195	2	C72252	conserved hypothet
955	60	5.4	234	2	S36116	proteasome endopat
956	60	5.4	237	2	C95199	nitroreductase fam
957	60	5.4	235	2	H81302	probable membrane
958	60	5.4	274	2	A47639	Ox-2 membrane glyc
959	60	5.4	277	2	F63401	bactetracin resista
960	60	5.4	283	2	S27708	daunorubicin resis
961	60	5.4	285	2	D27105	hypothetical prote
962	60	5.4	286	2	F82881	hypothetical prote
963	60	5.4	288	2	T43353	nuclear receptor N
964	60	5.4	292	2	F69372	osmoprotection pro
965	60	5.4	297	2	T48855	probable heat shoc
966	60	5.4	302	2	H84731	hypothetical prote
967	60	5.4	305	2	C97762	ABC transporter pe
968	60	5.4	312	2	C64494	hypothetical prote
969	60	5.4	312	2	D70643	hypothetical prote
970	60	5.4	314	2	T21003	hypothetical prote
971	60	5.4	319	2	T33261	hypothetical prote
972	60	5.4	323	2	T27640	hypothetical prote
973	60	5.4	325	2	F86605	sulfite synthetase/
974	60	5.4	325	2	C72020	3'-(2',5'-bisphosp
975	60	5.4	329	2	T07401	peroxidase (EC 1.1
976	60	5.4	329	2	A40730	class I histocompa
977	60	5.4	331	2	C97493	malonyl-CoA-acyl c
978	60	5.4	331	2	AE2711	malonyl-CoA:acyl c

979	60	5.4	341	2	B75264	1052	60	5.4	1736	2	A29176	sex-limited protei
980	60	5.4	343	2	T01475	1053	60	5.4	1803	2	S56894	YbB protein - yeas
981	60	5.4	346	2	B86715	1054	60	5.4	2206	2	G71611	hypothetical prote
982	60	5.4	355	2	AG4138	1055	60	5.4	2319	2	A47004	coagulation factor
983	60	5.4	363	2	T28726	1056	60	5.4	2523	2	T18477	hypothetical prote
984	60	5.4	364	2	AG0581	1057	60	5.4	3011	1	S40770	genome polyprotein
985	60	5.4	367	2	T22821	1058	59.5	5.4	37	2	B45875	Tta class I histoc
986	60	5.4	376	2	AF1943	1059	59.5	5.4	98	2	G81251	NADH2 dehydrogenas
987	60	5.4	397	2	D83311	1060	59.5	5.4	102	2	B34770	ORF2 protein - sai
988	60	5.4	406	2	T52647	1061	59.5	5.4	118	2	H90030	hypothetical prote
989	60	5.4	412	2	T05703	1062	59.5	5.4	141	2	B41563	integrin alpha-3A
990	60	5.4	413	2	B83180	1063	59.5	5.4	167	2	S14969	pathogenesis-relat
991	60	5.4	413	2	T34117	1064	59.5	5.4	179	2	T22143	hypothetical prote
992	60	5.4	414	2	B81413	1065	59.5	5.4	215	2	F96977	probable phosphata
993	60	5.4	415	2	T05705	1066	59.5	5.4	223	2	T19793	hypothetical prote
994	60	5.4	423	2	S39830	1067	59.5	5.4	231	2	A49485	flt3/Flk-2 ligand
995	60	5.4	428	2	C96633	1068	59.5	5.4	235	2	I38440	flt3 ligand - huma
996	60	5.4	443	2	T15704	1069	59.5	5.4	236	2	AB3628	transcription regu
997	60	5.4	452	2	T11108	1070	59.5	5.4	237	2	C96737	unknown protein f3
998	60	5.4	490	2	AG4215	1071	59.5	5.4	237	2	C81291	probable integrin
999	60	5.4	500	2	AE2032	1072	59.5	5.4	247	2	D24706	modulation protein
1000	60	5.4	511	2	T27716	1073	59.5	5.4	247	2	H95319	phosphoadenylyl-su
1001	60	5.4	512	2	B90442	1074	59.5	5.4	267	2	I55686	IGL-1 - mouse
1002	60	5.4	519	2	H96661	1075	59.5	5.4	280	2	I55577	FC gamma (IGG) rec
1003	60	5.4	527	2	AE3467	1076	59.5	5.4	282	2	F90437	hypothetical prote
1004	60	5.4	537	2	T33955	1077	59.5	5.4	302	2	F70220	conserved hypotnet
1005	60	5.4	540	2	G90068	1078	59.5	5.4	312	2	T18664	hypothetical 34.1K
1006	60	5.4	548	2	B90446	1079	59.5	5.4	312	2	H91237	hypothetical prote
1007	60	5.4	549	2	T16769	1080	59.5	5.4	312	2	D86085	hypothetical prote
1008	60	5.4	582	2	A36150	1081	59.5	5.4	320	2	JI0118	FC gamma (IGG) rec
1009	60	5.4	595	2	BE9470	1082	59.5	5.4	320	2	C88656	protein F56D6.5 [i
1010	60	5.4	600	2	T24626	1083	59.5	5.4	323	2	B64504	methenyltetrahydro
1011	60	5.4	628	2	AG1469	1084	59.5	5.4	326	2	S59101	NADH2 dehydrogenas
1012	60	5.4	676	2	T24550	1085	59.5	5.4	332	2	B86448	hypothetical prote
1013	60	5.4	687	2	S72932	1086	59.5	5.4	344	2	S62765	NADH2 dehydrogenas
1014	60	5.4	690	2	S75067	1087	59.5	5.4	345	1	QXMS2M	NADH2 dehydrogenas
1015	60	5.4	690	2	AB3441	1088	59.5	5.4	348	2	B64148	hypothetical prote
1016	60	5.4	696	2	AB1566	1089	59.5	5.4	359	2	HLH012	hypothetical prote
1017	60	5.4	703	2	BE9769	1090	59.5	5.4	360	2	T11639	MHC class I histoc
1018	60	5.4	711	2	A70624	1091	59.5	5.4	361	2	A75525	conserved hypotnet
1019	60	5.4	709	2	AB3897	1092	59.5	5.4	382	1	F70116	hypothetical prote
1020	60	5.4	718	2	T05850	1093	59.5	5.4	392	2	I54491	cell surface antiq
1021	60	5.4	756	2	AB1452	1094	59.5	5.4	398	2	S07145	triacylglycerol li
1022	60	5.4	769	2	T22316	1095	59.5	5.4	399	2	T27140	hypothetical prote
1023	60	5.4	773	2	T46059	1096	59.5	5.4	408	2	C71520	hypothetical prote
1024	60	5.4	784	2	T45697	1097	59.5	5.4	414	2	S48738	potassium channel
1025	60	5.4	792	2	T29187	1098	59.5	5.4	415	2	T08191	translactation elonga
1026	60	5.4	815	2	T15749	1099	59.5	5.4	419	2	B83904	hypothetical prote
1027	60	5.4	819	2	T40527	1100	59.5	5.4	424	2	H84134	multidrug resistan
1028	60	5.4	836	2	A90518	1101	59.5	5.4	425	2	S52852	inward rectifier p
1029	60	5.4	894	2	C86330	1102	59.5	5.4	427	2	D84540	hypothetical prote
1030	60	5.4	962	2	C43274	1103	59.5	5.4	427	2	G02034	Killer cell inhibi
1031	60	5.4	980	2	T49570	1104	59.5	5.4	428	2	T03251	calnexin - maize (
1032	60	5.4	995	2	T05842	1105	59.5	5.4	429	2	D82181	GGDEF family prote
1033	60	5.4	1013	2	C83771	1106	59.5	5.4	438	2	H91112	hypothetical prote
1034	60	5.4	1072	2	T17742	1107	59.5	5.4	438	2	H85957	peritall probable t
1035	60	5.4	1091	2	AA1543	1108	59.5	5.4	442	2	F87348	mannanase, probabl
1036	60	5.4	1108	2	AA4508	1109	59.5	5.4	442	2	S49741	probable membrane
1037	60	5.4	1136	2	A65559	1110	59.5	5.4	456	2	S69677	hypothetical prote
1038	60	5.4	1233	1	P3XR03	1111	59.5	5.4	457	2	T21063	hypothetical prote
1039	60	5.4	1234	2	A34911	1112	59.5	5.4	463	2	AH1513	amino acid transpo
1040	60	5.4	1237	2	A31789	1113	59.5	5.4	478	2	T32476	probable protein-c
1041	60	5.4	1241	2	T37150	1114	59.5	5.4	484	2	S73450	Glutamate-tRNA lig
1042	60	5.4	1250	1	B45219	1115	59.5	5.4	487	2	S65133	butyrophilin - mou
1043	60	5.4	1253	2	T21065	1116	59.5	5.4	501	2	B97790	app,ATP carrier pr
1044	60	5.4	1254	2	T18425	1117	59.5	5.4	502	2	T48241	ALK-1 - mouse
1045	60	5.4	1290	2	A56493	1118	59.5	5.4	502	2	TC4337	activin receptor
1046	60	5.4	1338	2	T18416	1119	59.5	5.4	515	2	S20449	probable maturase,
1047	60	5.4	1358	1	XOCHDH	1120	59.5	5.4	522	2	T28323	ORF MSV162 probabl
1048	60	5.4	1375	2	JT0345	1121	59.5	5.4	564	2	S73615	threonine-cRNA lig
1049	60	5.4	1465	2	S31262	1122	59.5	5.4	564	2	AG2823	ABC transporter, m
1050	60	5.4	1492	2	T18560	1123	59.5	5.4	564	2	F97601	atub (AE006182). [i
1051	60	5.4	1520	2	S46444	1124	59.5	5.4	579	2	T15135	hypothetical prote

1125	59.5	5.4	580	2	B38418	jockey protein 1 -	1198	59	5.4	337	2	AD1414	cytochrome P ubiqu
1126	59.5	5.4	581	2	T06825	ketol-acid reducto	1199	59	5.4	337	2	AC11790	cytochrome P ubiqu
1127	59.5	5.4	591	1	S30145	ketol-acid reducto	1200	59	5.4	345	2	A97252	sporulation protei
1128	59.5	5.4	591	2	T45681	ketol-acid reducto	1201	59	5.4	346	2	D97007	hypothetical prote
1129	59.5	5.4	606	2	T27072	hypothetical prote	1202	59	5.4	348	2	T21627	hypothetical prote
1130	59.5	5.4	618	2	S06446	citrolysin-related	1203	59	5.4	354	1	RGH02	GTP-binding regula
1131	59.5	5.4	621	1	D69295	endopoptidase La h	1204	59	5.4	358	2	FE4136	rtnd protein homol
1132	59.5	5.4	638	2	T37309	fil-1 protein - Ca	1205	59	5.4	366	2	A37374	Fc gamma (Igc) rec
1133	59.5	5.4	645	2	T28867	hypothetical prote	1206	59	5.4	372	2	G96973	probable membrane
1134	59.5	5.4	652	2	I48083	amphotropic murine	1207	59	5.4	372	2	AC3123	sugar acetylase (i
1135	59.5	5.4	675	2	F84937	DNA ligase (NAD) (	1208	59	5.4	372	2	D98164	hypothetical prote
1136	59.5	5.4	675	2	JC5898	beta-galactoside a	1209	59	5.4	381	2	B71700	DNA polymerase iii
1137	59.5	5.4	687	2	T29220	hypothetical prote	1210	59	5.4	388	2	I69644	O-antigen polymera
1138	59.5	5.4	688	2	T33708	hypothetical prote	1211	59	5.4	393	2	G71536	hypothetical prote
1139	59.5	5.4	730	2	T33041	hypothetical prote	1212	59	5.4	396	2	A36339	FL0 protein - gird
1140	59.5	5.4	730	2	B81217	organic solvent to	1213	59	5.4	403	2	T27948	hypothetical prote
1141	59.5	5.4	773	2	T46010	anthranilate phosph	1214	59	5.4	407	2	E88968	protein T2787.4 [i
1142	59.5	5.4	795	2	B97294	stage II sporulati	1215	59	5.4	418	2	A97220	probable membrane
1143	59.5	5.4	802	2	B81794	probable solvent t	1216	59	5.4	431	2	T52071	mRNA-binding prote
1144	59.5	5.4	823	2	A96501	hypothetical prote	1217	59	5.4	431	2	B98162	hypothetical prote
1145	59.5	5.4	824	2	A86783	glycosyl transfera	1218	59	5.4	431	2	T16191	hypothetical prote
1146	59.5	5.4	855	2	B75191	probable ATP-depen	1219	59	5.4	445	2	D69939	conserved hypothet
1147	59.5	5.4	864	2	T05945	lipoxygenase (EC 1	1220	59	5.4	447	2	A47430	gastrin/cholecysto
1148	59.5	5.4	897	1	A39255	cyclokin receptor	1221	59	5.4	449	2	D86557	D-Ala/Gly permease
1149	59.5	5.4	942	2	S23251	protein-tyrosine k	1222	59	5.4	452	2	A32067	d-ala/gly permease
1150	59.5	5.4	947	2	FXB12P	H+-exporting ATPas	1223	59	5.4	452	2	UC2459	gastrin/cholecysto
1151	59.5	5.4	974	2	T30204	pg12 protein - Str	1224	59	5.4	453	2	T24127	probable chitinase
1152	59.5	5.4	974	2	T35045	bacteriophage phiC	1225	59	5.4	455	2	E97081	amino acid permeas
1153	59.5	5.4	998	2	T04214	hypothetical prote	1226	59	5.4	467	2	AC1059	probable membrane
1154	59.5	5.4	1000	2	F70366	cation efflux (Acr	1227	59	5.4	482	2	AC1059	NADH2 dehydrogen
1155	59.5	5.4	1038	2	T31377	sog protein - fnu	1228	59	5.4	491	2	T22702	hypothetical prote
1156	59.5	5.4	1053	2	I55534	VLA-3 alpha subuni	1229	59	5.4	497	2	C75618	hypothetical prote
1157	59.5	5.4	1119	2	T18491	hypothetical prote	1230	59	5.4	498	2	AC0988	probable low-affin
1158	59.5	5.4	1145	2	T13810	DNA-directed DNA p	1231	59	5.4	501	2	T44298	sodium/proline sym
1159	59.5	5.4	1187	1	A53661	protein-tyrosine-p	1232	59	5.4	509	2	AO5183	hypothetical prote
1160	59.5	5.4	1188	2	C71231	hypothetical prote	1233	59	5.4	510	2	C85697	probable sporulati
1161	59.5	5.4	1199	2	T23005	hypothetical prote	1234	59	5.4	510	2	C90839	probable sporulati
1162	59.5	5.4	1276	2	B66776	hypothetical prote	1235	59	5.4	510	2	A64865	YGB protein - Bac
1163	59.5	5.4	1295	2	T12720	hypothetical prote	1236	59	5.4	532	1	TFBY	beta-fructofuranos
1164	59.5	5.4	1335	2	T18289	racGAP protein - s	1237	59	5.4	553	2	S64609	hypothetical prote
1165	59.5	5.4	1467	2	PC1253	leukocyte antigen-	1238	59	5.4	563	2	S21043	cytochrome b6 homo
1166	59.5	5.4	1497	1	TDBULK	hypothetical prote	1239	59	5.4	571	2	T39378	probable PAD bindi
1167	59.5	5.4	2391	2	G89779	conserved hypothet	1240	59	5.4	664	2	C47474	MDM-type ABC trans
1168	59.5	5.4	2491	2	A57036	apoptin - slime mold	1241	59	5.4	595	2	A10042	thiol-disulfide in
1169	59.5	5.4	2629	2	I46569	apoptin protein B -	1242	59	5.4	613	2	T47483	receptor like prot
1170	59.5	5.4	4488	1	RIHWM2	genome polyprotein	1243	59	5.4	623	2	T19876	hypothetical prote
1171	59.5	5.4	5147	1	IJFETM	cadherin-related t	1244	59	5.4	632	2	T45858	hypothetical prote
1172	59.5	5.4	118	2	F87479	conserved hypothet	1245	59	5.4	664	2	C90464	hypothetical prote
1173	59.5	5.4	189	1	LEPHUD	apoptin protein D p	1246	59	5.4	666	2	C90464	hypothetical prote
1174	59.5	5.4	202	2	T14970	phage lambda-relat	1247	59	5.4	670	2	T50312	hypothetical prote
1175	59.5	5.4	219	2	T29732	hypothetical prote	1248	59	5.4	695	2	S44049	nucleocapsid prote
1176	59.5	5.4	240	2	D64089	1-acylglycerol-3-p	1249	59	5.4	782	2	S33945	late protein, 100K
1177	59.5	5.4	243	2	A89907	hypothetical prote	1250	59	5.4	827	2	T39608	zinc finger trans
1178	59.5	5.4	247	2	E70137	hypothetical prote	1251	59	5.4	833	2	S19087	gene Delta protein
1179	59.5	5.4	248	2	B45831	cell division prot	1252	59	5.4	876	2	E89949	valine-tRNA ligase
1180	59.5	5.4	257	2	F86697	MHC class I histoc	1253	59	5.4	883	2	T18468	hypothetical prote
1181	59.5	5.4	260	2	B85181	hypothetical prote	1254	59	5.4	968	2	T39908	probable coiled co
1182	59.5	5.4	274	2	F96961	PC4 alpha and beta	1255	59	5.4	1275	2	S65824	reverse transcript
1183	59.5	5.4	285	2	T25971	bacitracin resista	1256	59	5.4	1323	2	S27224	N-methyl-D-aspart
1184	59.5	5.4	285	2	T24665	hypothetical prote	1257	59	5.4	1323	2	I78557	N-methyl-D-aspart
1185	59.5	5.4	289	2	B91042	hypothetical prote	1258	59	5.4	1352	2	G71051	probable ATP-depen
1186	59.5	5.4	289	2	A36964	N-acetylmuramoyl-1	1259	59	5.4	1356	1	CA5219	N-methyl-D-aspart
1187	59.5	5.4	289	2	E85886	N-acetylmuramoyl-L	1260	59	5.4	1472	2	A84470	hypothetical prote
1188	59.5	5.4	292	1	E64226	hypothetical prote	1261	59	5.4	1576	1	A23662	ipovosin I, high mol
1189	59.5	5.4	308	2	C81723	penicillin toleran	1262	59	5.4	1658	2	D86890	DNA-directed DNA p
1190	59.5	5.4	313	2	T33849	hypothetical prote	1263	59	5.4	1802	2	S52611	YB protein - yeas
1191	59.5	5.4	315	1	HNWZV	hemagglutinin prec	1264	59	5.4	2167	2	S19444	hypothetical prote
1192	59.5	5.4	318	1	F72171	K99 protein - vari	1265	59	5.4	4131	2	T21085	hypothetical prote
1193	59.5	5.4	323	1	QOBEED3	HHRF3 protein - hu	1266	59	5.4	4550	2	T18440	hypothetical prote
1194	59.5	5.4	323	2	UC2578	DNA repair protein	1267	59	5.3	162	2	T17051	hypothetical prote
1195	59.5	5.4	325	2	T33549	transcription regu	1268	59	5.3	162	2	T11802	NADH2 dehydrogen
1196	59.5	5.4	328	2	H87359	transcription regu	1269	59	5.3	176	2	AD0261	disulfide bond for
1197	59.5	5.4	329	2	T20094	hypothetical prote	1270	59	5.3	176	2	G69163	hypothetical prote

1271	58.5	5.3	181	1	B44057	early E3 20.3K gly	1344	58.5	5.3	425	2	B64491	type I restriction
1272	58.5	5.3	181	1	ERAD23	early E3 20.3K gly	1345	58.5	5.3	430	2	S15147	hypothetical prote
1273	58.5	5.3	184	2	A36290	let-60 ras protein	1346	58.5	5.3	443	2	H98093	hemolysin [impor
1274	58.5	5.3	189	2	AF0372	glycine cleavage s	1347	58.5	5.3	444	2	S41721	cell division cycl
1275	58.5	5.3	203	2	AC1395	hypothetical prote	1348	58.5	5.3	459	2	B70590	probable gorA prot
1276	58.5	5.3	237	2	AD1202	B. subtilis ynfP p	1349	58.5	5.3	467	2	T34617	Ndh2 dehydrogenas
1277	58.5	5.3	249	2	AE0118	hypothetical prote	1350	58.5	5.3	479	2	G90457	conserved b558/56
1278	58.5	5.3	250	2	H95161	conserved hypotnet	1351	58.5	5.3	481	2	B70179	cytochrome P450 71
1279	58.5	5.3	250	2	G98027	conserved hypotnet	1352	58.5	5.3	490	2	A86265	hypothetical prote
1280	58.5	5.3	252	2	AG1012	deer family regnla	1353	58.5	5.3	492	2	S75049	hypothetical prote
1281	58.5	5.3	254	2	T28266	ORF MSV105 hypotne	1354	58.5	5.3	505	2	B87021	probable integral-
1282	58.5	5.3	255	2	F84856	hypothetical prote	1355	58.5	5.3	519	2	F96517	hypothetical prote
1283	58.5	5.3	260	2	S07169	cytochrome-c oxida	1356	58.5	5.3	528	2	T31824	hypothetical prote
1284	58.5	5.3	264	2	G28969	N-carbamoylascosi	1357	58.5	5.3	538	2	T16034	hypothetical prote
1285	58.5	5.3	266	2	G64022	hypothetical prote	1358	58.5	5.3	546	2	T06415	calnexin - soybean
1286	58.5	5.3	270	2	S09898	hypothetical prote	1359	58.5	5.3	553	2	E91120	probable membrane
1287	58.5	5.3	272	2	GC4589	hypothetical prote	1360	58.5	5.3	553	2	E85965	probable membrane
1288	58.5	5.3	276	2	E97205	probable conserved	1361	58.5	5.3	555	2	A65093	hypothetical prote
1289	58.5	5.3	290	2	S55116	hypothetical prote	1362	58.5	5.3	555	2	T24671	hypothetical prote
1290	58.5	5.3	292	2	D71181	hypothetical prote	1363	58.5	5.3	556	2	G90352	thermopsin precurs
1291	58.5	5.3	296	2	D49539	xyloglucan endo-1,	1364	58.5	5.3	556	2	F82342	methyl-accepting c
1292	58.5	5.3	297	1	H64783	carbamate kinase (	1365	58.5	5.3	561	2	S63388	probable membrane
1293	58.5	5.3	303	2	A40807	membrane glycoprot	1366	58.5	5.3	570	2	AH1509	ABC transporter. A
1294	58.5	5.3	306	2	H87801	protein C10G11.3 [	1367	58.5	5.3	572	1	VGNZBA	cell fusion glycop
1295	58.5	5.3	310	1	HNVRRA	hemagglutinin prec	1368	58.5	5.3	574	1	VGNZBR	cell fusion glycop
1296	58.5	5.3	313	2	HQ1862	3JR protein - vari	1369	58.5	5.3	574	2	VGNZBS	cell fusion proteol
1297	58.5	5.3	313	2	G36854	hemagglutinin - va	1370	58.5	5.3	574	2	QJ1583	neopulvinase (BC
1298	58.5	5.3	313	2	T28598	hypothetical prote	1371	58.5	5.3	584	2	B86835	hnf-1/forkhead tra
1299	58.5	5.3	316	2	S26715	hypothetical prote	1372	58.5	5.3	586	2	JC6500	hypothetical prote
1300	58.5	5.3	317	2	C83652	hypothetical prote	1373	58.5	5.3	587	2	T46447	hypothetical prote
1301	58.5	5.3	327	2	S09566	replication initia	1374	58.5	5.3	588	2	H70618	probable p8 protei
1302	58.5	5.3	330	2	F83955	flagellar motor sw	1375	58.5	5.3	607	2	H87286	ABC transporter. H
1303	58.5	5.3	335	2	A24455	regB protein - Bac	1376	58.5	5.3	611	2	T21747	hypothetical prote
1304	58.5	5.3	335	2	A13111	hypothetical prote	1377	58.5	5.3	635	2	T22321	hypothetical prote
1305	58.5	5.3	335	2	D98175	hypothetical prote	1378	58.5	5.3	661	2	D69907	hypothetical prote
1306	58.5	5.3	340	2	T28767	hypothetical prote	1379	58.5	5.3	675	2	F85071	hypothetical prote
1307	58.5	5.3	343	2	AD1502	hypothetical prote	1380	58.5	5.3	711	1	ALBSXF	cyclomaldextrin
1308	58.5	5.3	344	1	RWRTC2	T-cell surfact gly	1381	58.5	5.3	712	2	S23650	retrovirus-related
1309	58.5	5.3	346	2	D85658	probable tellurium	1382	58.5	5.3	729	2	T16522	hypothetical prote
1310	58.5	5.3	346	2	B99798	probable tellurium	1383	58.5	5.3	750	2	B90137	sulfate permease [
1311	58.5	5.3	349	2	A53340	interferon regulat	1384	58.5	5.3	769	2	T49911	anthranilate phosp
1312	58.5	5.3	349	2	JC6311	interferon recepto	1385	58.5	5.3	770	2	T23999	hypothetical prote
1313	58.5	5.3	352	2	H64919	probable membrane	1386	58.5	5.3	778	2	G71418	hypothetical prote
1314	58.5	5.3	352	2	G85769	hypothetical prote	1387	58.5	5.3	783	2	S51968	probable membrane
1315	58.5	5.3	352	2	C90921	hypothetical prote	1388	58.5	5.3	795	2	S26712	hypothetical prote
1316	58.5	5.3	353	2	A87469	ubiquinol oxidase	1389	58.5	5.3	807	2	SS1460	hypothetical prote
1317	58.5	5.3	354	2	A83059	probable hemin deg	1390	58.5	5.3	822	2	C97211	uncharacterized co
1318	58.5	5.3	356	2	G76018	hypothetical prote	1391	58.5	5.3	848	2	G90128	elongation factor
1319	58.5	5.3	357	2	S11136	class I histocompa	1392	58.5	5.3	849	1	T09349	S-receptor kinase
1320	58.5	5.3	357	2	S11134	class I histocompa	1393	58.5	5.3	854	1	VCLJ51	env polyprotein pr
1321	58.5	5.3	357	2	S11137	class I histocompa	1394	58.5	5.3	874	1	QOBE15	BLuFI protein - hu
1322	58.5	5.3	357	2	S11140	class I histocompa	1395	58.5	5.3	879	2	T19199	hypothetical prote
1323	58.5	5.3	357	2	S11139	class I histocompa	1396	58.5	5.3	896	2	AE1514	conserved membrane
1324	58.5	5.3	357	2	S11135	class I histocompa	1397	58.5	5.3	911	1	B3HU	band 3 anion trans
1325	58.5	5.3	360	2	F90605	mannitol-1-phospha	1398	58.5	5.3	918	1	PXBYP	H+-exporting ATPas
1326	58.5	5.3	364	1	A64729	3-isopropylmalate	1399	58.5	5.3	956	2	T23570	hypothetical prote
1327	58.5	5.3	364	2	I72217	class I histocompa	1400	58.5	5.3	964	2	E70826	probable membrane
1328	58.5	5.3	365	2	172218	class I histocompa	1401	58.5	5.3	1030	2	T37868	probable helicase
1329	58.5	5.3	372	2	G01425	nucleolar 75K auto	1402	58.5	5.3	1131	2	F88570	protein K03H1.2 [i
1330	58.5	5.3	372	2	JE0087	delta opioid recep	1403	58.5	5.3	1144	2	T27408	hypothetical prote
1331	58.5	5.3	377	2	H71081	hypothetical prote	1404	58.5	5.3	1147	2	S64930	serine/threonine-s
1332	58.5	5.3	384	2	D97611	cell division prot	1405	58.5	5.3	1198	2	S51434	hypothetical prote
1333	58.5	5.3	384	2	AH2833	cell division prot	1406	58.5	5.3	1218	2	A88449	protein G28A5.2 [i
1334	58.5	5.3	384	2	AG0149	probable membrane	1407	58.5	5.3	1223	2	S43579	C28A5.1 protein (c
1335	58.5	5.3	393	2	E43674	u6e protein - huma	1408	58.5	5.3	1253	2	F86436	hypothetical prote
1336	58.5	5.3	393	2	B96780	hypothetical prote	1409	58.5	5.3	1280	2	T29021	hypothetical prote
1337	58.5	5.3	396	2	B91013	bicyclomyacin resis	1410	58.5	5.3	1407	1	EBWYML	TATA box-binding p
1338	58.5	5.3	396	2	D85857	bicyclomyacin resis	1411	58.5	5.3	1451	2	S41025	hypothetical prote
1339	58.5	5.3	405	2	D96917	probable permease	1412	58.5	5.3	1583	2	T00727	myosin heavy chain
1340	58.5	5.3	413	2	A95254	dlb protein limpo	1413	58.5	5.3	1717	2	T13961	DNA-directed RNA p
1341	58.5	5.3	414	2	B98119	hypothetical prote	1414	58.5	5.3	1753	2	S30855	hypothetical prote
1342	58.5	5.3	423	2	I38979	limar2 rectifier p	1415	58.5	5.3	2657	2	T18497	hypothetical prote
1343	58.5	5.3	423	2	I48202	potassium channel-	1416	58.5	5.3	4836	2	T14346	herc2 protein - mo

1417	58.5	5.3	4967	2	S7269	ryanodine receptor
1418	58.5	5.3	26926	1	I18344	titin, cardiac mms
1419	58	5.3	127	2	AG1425	hypothetical secre
1420	58	5.3	151	2	S48796	transforming prote
1421	58	5.3	153	2	A85848	hypothetical prote
1422	58	5.3	158	2	A27348	homeotic protein H
1423	58	5.3	171	2	C45665	adult-specific bru
1424	58	5.3	172	2	S52811	hypothetical prote
1425	58	5.3	172	2	A46775	major histocompati
1426	58	5.3	188	1	BVECTE	trial protein - Bsc
1427	58	5.3	199	2	H75531	cytochrome c-type
1428	58	5.3	214	2	H96842	F23A5.34 [imported]
1429	58	5.3	214	2	D96839	hypothetical prote
1430	58	5.3	218	2	AG3479	hypothetical prote
1431	58	5.3	218	2	T27678	hypothetical prote
1432	58	5.3	220	2	G90290	probable Deda-fam1
1433	58	5.3	232	2	AD0071	hypothetical prote
1434	58	5.3	237	2	H83719	hypothetical prote
1435	58	5.3	239	2	A69124	hypothetical prote
1436	58	5.3	244	2	AH0363	probable membrane
1437	58	5.3	246	2	AD3574	branched-chain am
1438	58	5.3	253	1	BVECC2	probable sulfate t
1439	58	5.3	253	2	H85883	required for sulfa
1440	58	5.3	253	2	E91039	required for sulfa
1441	58	5.3	254	2	C81846	hypothetical prote
1442	58	5.3	260	1	A46517	CD27 antigen precu
1443	58	5.3	266	1	A86467	hypothetical prote
1444	58	5.3	269	2	F70377	shikimate 5-dehydr
1445	58	5.3	272	2	S59389	probable membrane
1446	58	5.3	275	2	C97028	probable metal-bn
1447	58	5.3	279	2	AH1540	transcription regu
1448	58	5.3	281	2	E72395	sugar ABC transpor
1449	58	5.3	286	2	G83211	conserved hypochet
1450	58	5.3	289	2	T28922	hypothetical prote
1451	58	5.3	289	2	AG0812	probable N-acetylm
1452	58	5.3	289	2	AS3302	hem 5'-region hyp
1453	58	5.3	290	4	S07060	opsin, red-sensiti
1454	58	5.3	296	2	T07367	thioredoxin-like p
1455	58	5.3	297	2	E83194	polysamine transpor
1456	58	5.3	299	1	A69962	phosphate butyryl
1457	58	5.3	314	2	G69348	phosphate permease
1458	58	5.3	316	2	A11935	hypothetical prote
1459	58	5.3	320	2	D64205	putine-nucleoside
1460	58	5.3	323	2	A82433	fructokinase VC86
1461	58	5.3	332	2	A12107	hypothetical prote
1462	58	5.3	336	2	S35934	matrix protein - m
1463	58	5.3	338	2	H84972	ornithine carbamoy
1464	58	5.3	342	1	HLHUC4	MHC class I histoc
1465	58	5.3	350	1	A37963	complement C5a ana
1466	58	5.3	355	2	T50091	visual pigment - M
1467	58	5.3	361	2	T30085	hypothetical prote
1468	58	5.3	364	1	OOHUG	opsin, green-sensi
1469	58	5.3	366	2	T37078	HLA-C alpha chain
1470	58	5.3	370	2	T44667	chloromucinate cyc
1471	58	5.3	370	2	J00176	chloromucinate cyc
1472	58	5.3	370	2	C90465	3-hydroxycacyl-CoA
1473	58	5.3	377	2	B97376	cytochrome ba (3) (
1474	58	5.3	385	2	H86627	hypothetical prote
1475	58	5.3	393	2	D97979	hypothetical prote
1476	58	5.3	394	2	H64448	polyferredoxin - M
1477	58	5.3	397	2	T48717	proteinase inhibit
1478	58	5.3	398	2	A99452	acyl-CoA dehydrog
1479	58	5.3	399	2	E86480	43-6k hypochetral
1480	58	5.3	409	2	G83871	multidrug-efflux t
1481	58	5.3	409	2	E97218	GGDEF domain conta
1482	58	5.3	409	2	T19688	hypothetical prote
1483	58	5.3	410	2	D91291	probable transport
1484	58	5.3	410	2	F66132	probable transport
1485	58	5.3	418	2	A97300	gamma-glutamyl pho
1486	58	5.3	419	2	S46077	K(ATP) channel - r
1487	58	5.3	430	2	D86611	poly A polymerase
1488	58	5.3	430	2	C81526	poly(A) polymerase
1489	58	5.3	439	2	C69392	hypothetical prote

1490	58	5.3	440	2	JL0144	interleukin-6 rece
1491	58	5.3	442	2	T04815	hypothetical prote
1492	58	5.3	447	2	T00425	phicolase/blue-1i
1493	58	5.3	449	2	E87801	protein C10G11.6 (
1494	58	5.3	450	2	JQ1614	gastrin receptor -
1495	58	5.3	452	2	A46195	cholecystokinin B
1496	58	5.3	452	2	A85815	probable 2-compone
1497	58	5.3	452	2	B90967	probable 2-compone
1498	58	5.3	452	2	T00113	undecaprenyl-phosp
1499	58	5.3	452	2	C88969	protein F15E11.8 (
1500	58	5.3	453	2	S32817	gastrin receptor -

## ALIGNMENTS

## RESULT 1

T14762  
hypothetical protein DKFZp434A014.1 - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T14762

R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

A:Reference number: 218181

A:Accession: T14762

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-804 <MAN>

A:Cross-references: UNIPROT:Q9UF26; EMBL:AL110224

A:Experimental source: adult testis; clone DKFZp434A014

A:Note: DKFZp434A014.1

Query Match 34.1%; Score 376; DB 2; Length 804;

Best Local Similarity 47.9%; Pred. No. 1.8e-26;

Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY	19	PEAENAFKVRISIRALGDKAYAWDTNEEYLFKMANVASMR---KVPRERT-ELSHVL	73
DB	611	PYADQISIVRISLTKALDCKAYEMNDNEMYLFERSVAYAMROYFLKVNQMILFGSEEDVR	670
QY	74	LCNVTQVSPFWVVTDPSEK-NHTLPAYEVQSAIRNNKORINNAPFLNDOTLEFLKIPSTL	132
DB	671	VANLKRISFNFVPAKNVSDIIPRTVERKAIKRSKRINDAFRLNDSLEFLGIQPTL	730
QY	133	APPMDPSVPIWIIIFGVIFCIIVAIALLISGIWQRRKNKPS	177
DB	731	GPPNQPPVSIWLVGVVGVIVGIVILFVGIRDKKNKARS	775

## RESULT 2

T18523  
integrin alpha chain - Geodia cydonium

C:Species: Geodia cydonium  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T18523

R:pancer, Z.; Kruse, M.; Mueller, I.; Mueller, W.E.G.

Mol. Biol. Evol. 14, 391-398, 1997

A:Title: On the origin of adhesion receptors of metazoa: Cloning of the integrin alpha s

A:Reference number: 218946; MUID:97254987; PMID:9100369

A:Accession: T18523

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1086 <PAN>

A:Cross-references: UNIPROT:O18428; EMBL:X97283; PIDN:CAA65943.1

C:Function:

A:Description: signal transduction

C:Superfamily: integrin alpha-4 chain

Query Match 8.8%; Score 97.5; DB 2; Length 1086;  
Best Local Similarity 25.5%; Pred. No. 0.94;  
Matches 36; Conservative 24; Mismatches 52; Indels 29; Gaps 6;





Qy 95 TLPAVEVQSAIRMNKRNINNAFLUNDQLEFLKIPSTL 132  
Db 132 TL--VDVIGAL--VNVGIVMTNT--ASNENDMAGFKLPFTI 165

## RESULT 6

D38992  
C:Species: Homo sapiens (man)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000  
C/Accession: D38992  
R/Suzuki, S.; Sano, K.; Tanihara, H.  
Cell Regul. 2, 261-270, 1991  
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t  
A:Reference number: S24305; MUID:91283540; PMID:2059658  
A/Accession: D38992  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-793 <SUZ>  
A/Cross-references: GB:IJ3060; NID:G506411; PIDN:AAA35628.1; PID:G506412  
C/Genetics:  
A/Gene: GDB:CDH8  
A/Cross-references: GDB:5822911  
C/Superfamily: cadherin; cadherin repeat homology  
C/Keywords: calcium binding; cell adhesion; duplication  
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 8.1%; Score 89.5; DB 2; Length 793;  
Best Local Similarity 20.6%; Pred. No. 3.6;  
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

Qy 13 HAEICQPAENAFKVRSLRITLGDKAYAMPT-----NEEYLFKAMVAFSRKYPN 63  
Db 425 HTDERQFINADGKTLATPLDRELSVWNTITATEIRNHSQISVPAIKVLDV-N 483  
Qy 64 REATEIS--HVLIC-----NVTQVSPFWFVTPDPSKNH-----TLPAVEVQSAIRMNK 109  
Db 484 DNAEPFASVEYAFPCENKPGQVITQVSA-MDKODPKNGHFLVSLPDEMNNPFTIKK 542  
Qy 110 NRINNAFL-----NDQTEFLKIPSTLA---PPMDSPVPIWIIIFG----- 148  
Db 543 NEDNSLSTLAKNGFNRRQKEVYLLPIIISDGNPPLSSTSTLTITRVCGSNDGVQSCN 602  
Qy 149 -----VIFCIITVATALLLSGIMQRRKRSSEVDADKCEMMIT 191  
Db 603 VEAYVLPGLSMGALLATLACITILLVIVLF--VTLRRHQKNEPLIKDDEVDRENTIR 660  
Qy 192 IEN 194  
Db 661 YDD 663

## RESULT 7

T13933  
pol polyprotein - fruit fly (Drosophila virilis) retrotransposon Tv1 (fragment)  
C:Species: Drosophila virilis  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: T13933  
R/Andrianov, B.V.; Zakhar'yev, V.M.; Evgen'ev, M.B.; Schuppe, N.G.  
submitted to the EMBL Data Library, April 1998  
A/Description: Gypsy group retrotransposon Tv1 from Drosophila virilis.  
A/Reference number: Z17816  
A/Accession: T13933  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1188 <AND>  
A/Cross-references: UNIPROT:O76326; EMBL:AF056940; NID:G3493212; PID:G3493214; PIDN:AA3  
C/Genetics:  
A/Gene: pol  
A/Cross-references: FlyBase:FBgn0013099  
A/Mobile element: retrotransposon Tv1  
C/Superfamily: pol polyprotein

Query Match 8.1%; Score 89.5; DB 2; Length 1188;  
Best Local Similarity 24.8%; Pred. No. 5.7;  
Matches 34; Conservative 27; Mismatches 41; Indels 35; Gaps 7;

Qy 5 LEPLVTAIHAEICQPAENAFKVRSLRITLGDKAYAMPTNEEYLFKAMVAFSRKYPN 64  
Db 81 LNYQISPIHACTRPS-----RLTSRDSNSGGIRIDNIGKFL-----FSKREPRNR 127  
Qy 65 EAT-----EISHVLLCNV-----TORVSPFWFVTPDPSKNHTLPAV-EVQSAIR 106  
Db 128 NKSIRKWMIMELTFLKCIDVTGSTINIMKTRNLNF-FVNETLKVHTINGVIELKOSIR 186  
Qy 107 MNKNRI---NNAFLND 120  
Db 187 LGASTICPSKOKFTIHD 203

## RESULT 8

JC7294  
alphaP integrin - sea urchin (strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: JC7294  
R/Susan, J.M.; Just, M.L.; Lemarz, W.J.  
Biochem. Biophys. Res. Commun. 272, 929-935, 2000  
A:Title: Cloning and characterization of alphaP integrin in embryos of the sea urchin St  
A:Reference number: JC7294  
A/Contents: Embryo  
A/Accession: JC7294  
A/Molecule type: mRNA  
A/Residues: 1-1054 <SUS>  
A/Cross-references: UNIPROT:Q9U6S1; GB:AAD55724  
C/Genetics:  
A/Gene: eualphaP  
C/Superfamily: integrin alpha-2b chain  
C/Keywords: calcium binding; embryo; glycolysis; glycoprotein; heterodimer; transmembran

Query Match 8.1%; Score 89; DB 2; Length 1054;  
Best Local Similarity 20.5%; Pred. No. 5.5;  
Matches 56; Conservative 30; Mismatches 59; Indels 128; Gaps 13;

Qy 15 ELCPGAENAFKVRSLRITLGDKAYAM-----DTNEEYLF----- 50  
Db 795 EVRRYTGSSNAEVLNLNR-----WPEDENGDYILFYLLGIMTBGVTCQISQGAN 845  
Qy 51 -----KAMVAFSRKYPNRE-----ATEISHVLL--CNVQ--- 79  
Db 846 PLGVKLEASTKEQLSNTTQVSGRRKREGEYAEALAQAEPIFCYPPESCVLINTIDEIKA 905  
Qy 80 -----RV--SFWFVTPDPSKNHTLPAVEVQSAIRMNKRNINNAFLUNDQLEFLKIPST 131  
Db 906 TKSKRVVILGRFWERTQKAVSAVPIQVTLA-----STATATVRSIYN 951  
Qy 132 LAPPMD-----PSVPI--WIIIFVICIIIVATALLLSGIWQ--- 168  
Db 952 IPLPMEFTDSYKASTLTAEELVLPVPSIAWMIIVSVLGSITLL---LIILIGMKGF 1008  
Qy 169 -RRRKNE-----PSEYDDAEK 185  
Db 1009 FERKKPEDQKEPVAVTEKDGPEVYADPR 1041

## RESULT 9

A37009  
CD44 homolog membrane glycoprotein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 09-Jul-2004  
C/Accession: A37009  
R/Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.  
J. Immunol. 143, 3390-3395, 1999  
A:Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CAM  
A/Reference number: A37009; MUID:90038499; PMID:2681436  
A/Accession: A37009



Query Match 7.8%; Score 85.5; DB 2; Length 667;  
 Best Local Similarity 21.6%; Pred. No. 6.8;  
 Matches 37; Conservative 23; Mismatches 64; Indels 47; Gaps 6;

QY 81 VSFVFWVDPSPKNTLPAVEVQSAR-----MKNRINNAFF 117  
 DB 192 VQWVIDVGSLLNTLAIETQKPRKPLISRDINSEIFQDKMTIGSGSNRLTSNXYI 251

QY 118 LN-----DQTLFELKISTLAP-----PMDSPVPIWIIIFGVIFCIIVALL 161  
 DB 252 LGMFSKSKERFQSGIDLSKLPQAPIPRNEQA VPRBEKKKLPILIGV--ILAVIPYLM 309

QY 162 ILSGI-WRRRKKEPSEVDAAE-----DKENMTTENGIPSDPLMKKG 206  
 DB 310 VLGGVWYRRKKYAEVKSWEKYGPHRYSTKYLKATNGFVKALVKGKG 360

## RESULT 14

probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C/Accession: B81924

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holtroyd, S.; Jogle, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajadream,  
 Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: B81924

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-468 <PAR>

A/Cross-references: UNIPROT:Q9JVK7; GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB8408

A/Experimental source: serogroup A, strain 22491

C/Genetics:

A/Gene: NMA0797

C/Keywords: phosphotransferase

Query Match 7.7%; Score 84.5; DB 2; Length 468;  
 Best Local Similarity 23.7%; Pred. No. 5.5;  
 Matches 47; Conservative 29; Mismatches 81; Indels 41; Gaps 9;

QY 21 AENAFAKRLSIRTL-----GDKAYADTNEEYLFKAMVAFSMKRVPRREATEI 69  
 DB 34 AENPNORRTLETLMGSIISAFRARGD-AGARELTETWK-DSVSSGVYVIQDEKDI 91

QY 70 SHVLICNVTORVSEFWFVVTDPKNTLPAVEVQSARINNKRRINN--AFPLND-OTLEFL 126  
 DB 92 LHRITDSTIRALFLAAGHPSN-----LVHIEYRFGSEYLFTRKMDKQAR 141

QY 127 KIPSTLAPMDPSVPIW-----IIIFGVIFCIIV--VALALLISGIWQR---RR 171  
 DB 142 RLPSPLILPGPLAPIWHELIIISFIIIVGLMAYIAGNIAPRIILGNGMDRVANGEL 201

QY 172 KNKPSSEVDADCEM 189  
 DB 202 ETRISQVDDRDDELSHL 219

## RESULT 15

JG0022

flagellar basal-body M-ring protein flif - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 09-Jul-2004

C/Accession: JG0022; A42365; B69624; S14494

R:Zuber, A.R.; Ying, C.; Blechhoff, D.S.; Ordal, G.W.

Gene 101, 23-31, 1991

A/Title: Gene-protein relationships in the flagellar hook-basal body complex of Bacillus

A/Reference number: JG0019; MUID:91285431; PMID:1905667

A/Accession: JG0022

A/Molecule type: DNA

A/Residues: 1-536 <ZUB>

A/Cross-references: UNIPROT:P23447; GB:M54965

R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.

J. Bacteriol. 173, 3573-3579, 1991

A/Title: The flia locus of Bacillus subtilis is part of a large operon coding for flagel

A/Reference number: A42365; MUID:91258343; PMID:1828465

A/Accession: A42365

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 355-536 <ALB>

A/Cross-references: GB:M72718; EMBL:X56049; NID:939904; PIDN:CAA39520.1; PID:G3979709

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bester

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

lech, J.; Harwood, C.R.; Henauc, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y. M.; Ogawa, K.; Ogilwara, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Sero

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetta, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A/Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9364377

A/Accession: B69624

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-536 <KUN>

A/Cross-references: GB:299112; GB:AL009126; NID:92633902; PIDN:CAB13494.1; PID:ell85212;

A/Experimental source: strain 168

C/Genetics:

A/Gene: flif

Query Match 7.7%; Score 84.5; DB 2; Length 536;  
 Best Local Similarity 19.9%; Pred. No. 6.5;  
 Matches 39; Conservative 36; Mismatches 68; Indels 53; Gaps 8;

QY 9 VTAIHAELCOGAENAFKRLSIRTLADGKAYADTNEEYLFKAMVAFSMKRVPRREATE 68  
 DB 352 VNRHKEI-----AASPYKVR-----DLGIQVWVEPPDAKNTASLSTERODD 393

QY 69 ISHVLICNVTORVSEFWFVVTDPKNTLPAVEVQSARINNKRRINN--AFPLND-OTLEFL 128  
 DB 394 IQKIL-STVVRTS--LDKETONQNSDADINNKIVASVQPDGKYNLDTNTEE--- 444

QY 129 PSTLAPMDPSVPIW-IIIFGVIFCIIVALLILSGIWMQR---RR 171  
 DB 445 -----SSGIPLMAYIVGVLLAIIIVLIMLI-----RKKRQADEFEFEYEY- 487

QY 188 NMITTEGIPSDPLDM 203  
 DB 488 -----VPOEPINL 495

Search completed: August 18, 2005, 17:34:15  
 Job time : 42 secs

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GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: August 18, 2005, 17:27:03 ; Search time 72 Seconds  
(without alignment)  
1138.794 Million cell updates/sec

Title: US-09-997-641-387  
Perfect score: 1102  
Sequence: 1 MLLVLFVTAHAEICPG.....ENGIPSDPLDKGILMMP 212  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq.16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6751	standard; protein; 212 AA.				
DE	Membrane-bound protein PRO1312.					
PN	WO9663088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 3;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 2						
ID	AAB3447	standard; protein; 212 AA.				
DE	Human PRO1312 protein UNQ678 SEQ ID NO:161.					
PN	WO200053758-A2.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 3;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 3						
ID	AAB24430	standard; protein; 212 AA.				
DE	Human PRO1312 protein sequence SEQ ID NO:214.					
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 3;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 4						
ID	AAU12412	standard; protein; 212 AA.				
DE	Human PRO1312 polypeptide sequence.					
PN	WO200140466-A2.					
PD	07-JUN-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 4;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 5						
ID	AAB65274	standard; protein; 212 AA.				
DE	Human PRO1312 (UNQ678) protein sequence SEQ ID NO:387.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 4;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 6						
ID	ABU58089	standard; protein; 212 AA.				

DE	Human PRO polypeptide #121.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 7						
ID	ABU59167	standard; protein; 212 AA.				
DE	Novel human secreted or transmembrane protein PRO1312.					
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 8						
ID	ABU82679	standard; protein; 212 AA.				
DE	Human secreted/transmembrane protein PRO1312.					
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 9						
ID	ABO17856	standard; protein; 212 AA.				
DE	Novel human secreted and transmembrane protein PRO1312.					
PN	US2003032156-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 10						
ID	ABU60598	standard; protein; 212 AA.				
DE	Human secreted/transmembrane protein, #157.					
PN	US2002160384-A1.					
PD	31-OCT-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 11						
ID	ABU13980	standard; protein; 212 AA.				
DE	Human PRO1312 polypeptide.					
PN	US2002103125-A1.					
PD	01-AUG-2002.					
PA	(GETH ) GENENTECH LTD.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 12						
ID	ABU81110	standard; protein; 212 AA.				
DE	Human PRO polypeptide #241.					
PN	US2003004311-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 13						
ID	ABU72565	standard; protein; 212 AA.				
DE	Novel human secreted and transmembrane protein PRO1312.					
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 14						
ID	ABU66810	standard; protein; 212 AA.				
DE	Human PRO polypeptide #241.					
PN	US2003036180-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1102;	DB 6;	Length 212;		
Best Local Similarity	100.0%;	Pred. No. 8e-114;				
RESULT 15						
ID	ABU59891	standard; protein; 212 AA.				
DE	Novel secreted and transmembrane protein PRO1312.					
PN	US2003017563-A1.					
PD	23-JAN-2003.					

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 16  
ID ABUS9314 standard; protein, 212 AA.  
DE Human secreted/transmembrane protein, #157.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 17  
ID ABO26011 standard; protein, 212 AA.  
DE Human PRO1312 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 18  
ID ABO25081 standard; protein, 212 AA.  
DE Human secreted/transmembrane protein (PRO) #241.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 19  
ID ABUS9020 standard; protein, 212 AA.  
DE Human secreted/transmembrane protein, #157.  
PN US2002142861-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 20  
ID ABUS9298 standard; protein, 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 21  
ID ABUS9463 standard; protein, 212 AA.  
DE Novel human secreted and transmembrane protein PRO1192.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 22  
ID ABUS67086 standard; protein, 212 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 482.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 23  
ID ABUS9229 standard; protein, 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 24  
ID ABUS10935 standard; protein, 212 AA.  
DE Human PRO polypeptide #121.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 25  
ID ABUS1687 standard; protein, 212 AA.

DE Novel human secreted and transmembrane protein PRO1312.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 26  
ID ABUS8626 standard; protein, 212 AA.  
DE Human secreted and transmembrane polypeptide PRO1312.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 27  
ID ABO34140 standard; protein, 212 AA.  
DE Human PRO1312 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 28  
ID ADA4601 standard; protein, 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 29  
ID ADA76432 standard; protein, 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 30  
ID ADA19082 standard; protein, 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 31  
ID ADA61705 standard; protein, 212 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 32  
ID ADB19490 standard; protein, 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 33  
ID ADB28031 standard; protein, 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 34  
ID ADA86510 standard; protein, 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082711-A1.

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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 35
ID ADB16074 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 36
ID ADA37898 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 37
ID ADA47860 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 38
ID ADA21584 standard; protein; 212 AA.
DE Human secreted/transmembrane polypeptide PRO1312.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 39
ID ADA10371 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 40
ID ADA67655 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 41
ID ADB30662 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 42
ID ADA85958 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 43
ID ADA17915 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 44
ID ADA97170 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 45
ID ADA79474 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 46
ID ADA87613 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 47
ID ADB16815 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 48
ID ADA28023 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 49
ID ADA91907 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 50
ID ADB14970 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 51
ID ADB18931 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 52
ID ADA94146 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 53
ID ADB20042 standard; protein; 212 AA.
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DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 54  
ID ADB13354 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 55  
ID ABO43389 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 56  
ID ADA94603 standard; protein: 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 57  
ID ADA74608 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 58  
ID ADB24841 standard; protein: 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 59  
ID ADA82365 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 60  
ID ADA75328 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 61  
ID ADA85406 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 62  
ID ADA84854 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082708-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 63  
ID ADB30110 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 64  
ID ADA80638 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 65  
ID ADA75680 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 66  
ID ADA38828 standard; protein: 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 67  
ID ADA47105 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 68  
ID ADB25401 standard; protein: 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 69  
ID ADA93577 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 70  
ID ADB26927 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 71  
ID ADB31214 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.



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Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 72
ID ADA2949 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 73
ID ADA61142 standard; protein; 212 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 74
ID ADB24289 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077714-A1.
PD 24-APR-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 75
ID ADA96618 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082690-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 76
ID ADA61190 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082702-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 77
ID ADA6066 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082759-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 78
ID ADB26375 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082760-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 79
ID ADB21860 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082765-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 80
ID ADA77639 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068797-A1.
PD 10-APR-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 81
ID ADB18379 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077710-A1.
PD 24-APR-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 82
ID ADA87062 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082709-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 83
ID ADA8165 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082700-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 84
ID ADA6553 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003054516-A1.
PD 20-MAR-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 85
ID ADB28583 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082699-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 86
ID ADB29135 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082706-A1.
PD 01-MAY-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 87
ID ABO53226 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 88
ID ADA77087 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003059909-A1.
PD 27-MAR-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 89
ID ADA22510 standard; protein; 212 AA.
DE Human secreted/transmembrane polypeptide PRO1312.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match          100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 90
ID ADA88717 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
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PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 91  
ID ADA97722 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 92  
ID ADB27479 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 93  
ID ADB22412 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 94  
ID ABO22596 standard; protein: 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 95  
ID ADX06676 standard; protein: 212 AA.  
DE Human secreted/transmembrane PRO polypeptide #121.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 96  
ID ADA39369 standard; protein: 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 97  
ID ADA67103 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 98  
ID ADB22964 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 99  
ID ADB23737 standard; protein: 212 AA.  
DE Human PRO polypeptide SEQ ID NO 462.  
PN US200307712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 100

ID ADA92459 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 101  
ID ADB15522 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 102  
ID ADB38774 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 103  
ID ADB96395 standard; protein: 212 AA.  
DE Human PRO polypeptide #121.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 104  
ID ADB38222 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 105  
ID ADB66694 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 106  
ID ADB89774 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 107  
ID ADB90506 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 108  
ID ADB39607 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 109  
ID ADB47230 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.

PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 110  
ID ADB86837 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 111  
ID ADB77442 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 112  
ID ADB34599 standard; protein; 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 113  
ID ADB35703 standard; protein; 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 114  
ID ADB34047 standard; protein; 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 115  
ID ADB35151 standard; protein; 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 116  
ID ADB36255 standard; protein; 212 AA.  
DE Human PRO polypeptide SEQ ID NO 482.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 117  
ID ADB46650 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 118  
ID ADC57867 standard; protein; 212 AA.  
DE Human PRO polypeptide #121.  
PN US2003027754-A1.

PD 06-FEB-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 119  
ID ADC55231 standard; protein; 212 AA.  
DE Human PRO polypeptide #121.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 120  
ID ADC12098 standard; protein; 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 121  
ID ADC56520 standard; protein; 212 AA.  
DE Human PRO polypeptide #121.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 122  
ID ADC07575 standard; protein; 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 123  
ID ADC11565 standard; protein; 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 124  
ID ADC50523 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 125  
ID ADC72070 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 126  
ID ADC60049 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 127  
ID ADC53056 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein Seq ID482.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 128  
ID ADC57410 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein Seq ID482.

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PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 129
ID ADC60601 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 130
ID ADC51076 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 131
ID ADC65603 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 132
ID ADC54701 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 133
ID ADC53662 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 134
ID ADC59185 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 135
ID ADC56063 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 136
ID ADC58633 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 137
ID ADC14667 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 138
ID ADD08219 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US200306623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 139
ID ADD03307 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 140
ID ADC90299 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 141
ID ADC82044 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 142
ID ADC69718 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 143
ID ADC48607 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 144
ID ADD10136 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 145
ID ADD07686 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 146
ID ADD04711 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
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RESULT 147
ID  ADC82577 standard; protein; 212 AA.
DE  Human PRO polypeptide #121.
PN  US2003059833-A1.
PD  27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 148
ID  ADC80667 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2003092103-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 149
ID  ADD11174 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003194774-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 150
ID  ADC48055 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003194771-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 151
ID  ADD08757 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2003073090-A1.
PD  17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 152
ID  ADC80115 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2003087358-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 153
ID  ADD07006 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2002193100-A1.
PD  19-DEC-2002.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 154
ID  ADD09584 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003194775-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 155
ID  ADC83253 standard; protein; 212 AA.
DE  Human PRO polypeptide #121.
PN  US2003059783-A1.
PD  27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 156
ID  ADD41297 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2003203438-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 157
ID  ADD52436 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003194769-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 158
ID  ADD53176 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003194792-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 159
ID  ADD53728 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2003203437-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 160
ID  ADD55360 standard; protein; 212 AA.
DE  Human PRO polypeptide #121.
PN  US2003077593-A1.
PD  24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 161
ID  ADD56315 standard; protein; 212 AA.
DE  Human PRO polypeptide #121.
PN  US2003077594-A1.
PD  24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 162
ID  ADD51884 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003194779-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 163
ID  ADD02683 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003203431-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 164
ID  ADD02117 standard; protein; 212 AA.
DE  Human PRO polypeptide #241.
PN  US2003203430-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
RESULT 165
ID  ADD54299 standard; protein; 212 AA.
DE  Novel human secreted and transmembrane protein PRO1312.
PN  US2003203432-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1102; DB 7; Length 212;
Pred. No. 8e-114;
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Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 166  
ID ADE54756 standard; protein: 212 AA.  
DE Human PRO polypeptide #121.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 167  
ID ADE92616 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 168  
ID ADE91512 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 169  
ID ADE04126 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 170  
ID ADE26910 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 171  
ID ADE32423 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 172  
ID ADE22355 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 173  
ID ADE79579 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 174  
ID ADE42115 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 175

ID ADE17932 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 176  
ID ADE92064 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 177  
ID ADE33527 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 178  
ID ADE34079 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 179  
ID ADE80131 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 180  
ID ADE93168 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 181  
ID ADE19588 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 182  
ID ADE19036 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 183  
ID ADE43232 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 184  
ID ADE96021 standard; protein: 212 AA.

DE Human PRO polypeptide #241.  
PN US2003199059-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 185  
ID ADE32907 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 186  
ID ADE79025 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 187  
ID ADE26377 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 188  
ID ADE32975 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 189  
ID ADE42667 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 190  
ID ADE80683 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 191  
ID ADE89711 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 192  
ID ADE40995 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 193  
ID ADE04794 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199034-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 194  
ID ADE92923 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 195  
ID ADE7314 standard; protein; 212 AA.  
DE Human PRO1312 amino acid sequence SEQ ID NO.387.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 196  
ID ADE21632 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 197  
ID ADE32273 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 198  
ID ADE97608 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 199  
ID ADE80672 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 200  
ID ADE80120 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 201  
ID ADE55412 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 202  
ID ADE55964 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207379-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 203  
ID ADI35568 standard; protein; 212 AA.  
DE Human PRO polypeptide #121.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 204  
ID ADI64183 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 205  
ID ADI65132 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 206  
ID ADI63631 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 207  
ID ADH82045 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 208  
ID ADI00061 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 209  
ID ADH81493 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 210  
ID ADM82662 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 211  
ID ADI16061 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 212  
ID ADN16690 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 213  
ID ADN15509 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 214  
ID ADN14957 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 215  
ID ADC81219 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 216  
ID ADD76667 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 217  
ID ADD86031 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 218  
ID ADD86435 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 219  
ID ADE75883 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 220  
ID ADE23459 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 221



ID ADE24011 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 222  
ID ADE24654 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 223  
ID ADE87479 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 224  
ID ADE89345 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 225  
ID ADE18484 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 226  
ID ADE88793 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 227  
ID ADE94813 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 228  
ID ADE91224 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 229  
ID ADE35513 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 230  
ID ADE95365 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.

PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 231  
ID ADE93475 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199050-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 232  
ID ADE35056 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 233  
ID ADE92371 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 234  
ID ADE90672 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 235  
ID ADE91819 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 236  
ID ADE11763 standard; protein; 212 AA.  
DE Human PRO1312 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 237  
ID ADE902398 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 238  
ID ADE922184 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 239  
ID ADE920254 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207376-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 240  
ID ADF98160 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 241  
ID ADG24377 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 242  
ID ADF98731 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 243  
ID ADG03562 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 244  
ID ADF99283 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 245  
ID ADG16868 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 246  
ID ADG05327 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 247  
ID ADG19594 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 248  
ID ADG13431 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 249  
ID ADG08488 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 250  
ID ADG15658 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 251  
ID ADF97056 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 252  
ID ADG06241 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 253  
ID ADG23825 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 254  
ID ADG04114 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 255  
ID ADG25015 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 256  
ID ADG07312 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 257  
ID ADG07864 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 258  
ID ADG5359 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 259  
ID ADG6103 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 260  
ID ADG62127 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 261  
ID ADG62328 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 262  
ID ADG57567 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 263  
ID ADG57015 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 264  
ID ADG55911 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 265  
ID ADG58671 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 266  
ID ADG71037 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;

Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 267  
ID ADG58119 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 268  
ID ADG53703 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 269  
ID ADG71589 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 270  
ID ADG61776 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 271  
ID ADH19633 standard; protein; 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 272  
ID ADH30738 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 273  
ID ADH12105 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 274  
ID ADG52527 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 275  
ID ADG54255 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 276

ID ADG81224 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 277  
ID ADG556463 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 278  
ID ADH12729 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 279  
ID ADH21126 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 280  
ID ADG61575 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 281  
ID ADH20166 standard; protein: 212 AA.  
DE Human secreted/transmembrane protein PRO1312.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 282  
ID ADH28662 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 283  
ID ADG554807 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 284  
ID ADG59647 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 285  
ID ADH1271 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.

PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 286  
ID ADG10014 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 287  
ID ADH15485 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 288  
ID ADG09362 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 289  
ID ADH14817 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 290  
ID ADH18412 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 291  
ID ADH36369 standard; protein: 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 292  
ID ADH77588 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 293  
ID ADH65710 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 294  
ID ADM27846 standard; protein: 212 AA.  
DE Human PRO polypeptide #241.  
PN US2004048333-A1.

PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 295  
ID ADM42570 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 296  
ID ADM28432 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 297  
ID AD195914 standard; protein; 212 AA.  
DE Human PRO polypeptide #241.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 298  
ID AD16466 standard; protein; 212 AA.  
DE Novel human secreted and transmembrane protein PRO1312.  
PN US200307354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 299  
ID ADT94384 standard; protein; 212 AA.  
DE Human PRO1312 protein.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1102; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 8e-114;  
RESULT 300  
ID AAB88560 standard; protein; 222 AA.  
DE Human hydrophobic domain containing protein clone HP10720 #64.  
PN WO200112660-A2.  
PD 22-FEB-2001.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 97.4%; Score 1073; DB 4; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.4e-110;  
RESULT 301  
ID ADA56986 standard; protein; 222 AA.  
DE Human secreted protein #269.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.4%; Score 1073; DB 6; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.4e-110;  
RESULT 302  
ID ADA40837 standard; protein; 222 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.4%; Score 1073; DB 6; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.4e-110;  
RESULT 303  
ID ABR01796 standard; protein; 222 AA.  
DE Human cancer-related protein, 156PID4.  
PN WO200283921-A2.  
PA (GETH ) GENENTECH INC.  
Query Match 97.4%; Score 1073; DB 6; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.4e-110;  
RESULT 304  
ID AD11613 standard; protein; 222 AA.  
DE Human novel secreted protein, SEQ ID NO 141.  
PN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.4%; Score 1073; DB 6; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.4e-110;  
RESULT 305  
ID ADD37902 standard; protein; 222 AA.  
DE Human secreted protein #85.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.4%; Score 1073; DB 7; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.4e-110;  
RESULT 306  
ID AAW29670 standard; protein; 222 AA.  
DE Homo sapiens clone AM42\_3 secreted protein.  
PN WO9832853-A2.  
PD 30-JUL-1998.  
PA (GEMY ) GENETICS INST INC.  
Query Match 97.1%; Score 1070; DB 2; Length 222;  
Best Local Similarity 99.5%; Pred. No. 3.1e-110;  
RESULT 307  
ID ADE11757 standard; protein; 222 AA.  
DE Human secreted polypeptide #12.  
PN US2003100051-A1.  
PD 29-MAY-2003.  
PA (RUBE/) RUBEN S M.  
PA (FLO/) FLORENCE K A.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (CART/) CARTER K C.  
PA (MOOR/) MOORE P A.  
PA (OLSE/) OLSEN H S.  
PA (SHI/) SHI Y.  
PA (YOUN/) YOUNG P E.  
PA (WEI/) WEI Y.  
PA (BREM/) BREMER L A.  
PA (SOBP/) SOPPET D R.  
PA (LAF/) LAFLEUR D W.  
PA (ENDR/) ENDRESS G A.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 96.7%; Score 1066; DB 7; Length 222;  
Best Local Similarity 99.5%; Pred. No. 8.7e-110;  
RESULT 308  
ID AAY76135 standard; protein; 223 AA.  
DE Human secreted protein encoded by gene 12.  
PN WO9958660-A1.  
PD 18-NOV-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 96.7%; Score 1066; DB 3; Length 223;  
Best Local Similarity 99.5%; Pred. No. 8.7e-110;  
RESULT 309  
ID AAY04156 standard; protein; 222 AA.  
DE Human 5' EST secreted protein SEQ ID NO.27.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 310  
ID AAW93620 standard; protein; 222 AA.  
DE Human 5' EST secreted protein clone 58-35-2-F10-F12.  
PN WO9906551-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.

Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 311  
ID AAY35890 standard; protein: 222 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 27.  
PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 312  
ID AAY59653 standard; protein: 222 AA.  
DE Secreted protein extended EST protein sequence #6.  
PN WO9940189-A2.  
PD 12-AUG-1999.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 313  
ID AAY01594 standard; protein: 222 AA.  
DE Secreted protein encoded by an extended 5' EST cDNA sequence.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 314  
ID AAY12986 standard; protein: 222 AA.  
DE Human secreted protein encoded by 5' EST clone 58-35-2-F10-FL2.  
PN WO9906552-A2.  
PD 11-FEB-1999.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 315  
ID AAY25459 standard; protein: 222 AA.  
DE Human secreted protein 6 derived from extended cDNA.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 316  
ID AAY12680 standard; peptide: 222 AA.  
DE Human 5' EST secreted protein.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 2; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 317  
ID AAG00014 standard; protein: 222 AA.  
DE Human secreted protein #3.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GSEST ) GENSET.  
Query Match 95.1%; Score 1048; DB 3; Length 222;  
Best Local Similarity 98.1%; Pred. No. 8.7e-108;  
RESULT 318  
ID AAY04174 standard; protein: 222 AA.  
DE Human 5' EST secreted protein SEQ ID NO:27.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GSEST ) GENSET.  
Query Match 94.4%; Score 1040; DB 2; Length 222;  
Best Local Similarity 97.6%; Pred. No. 6.8e-107;  
RESULT 319  
ID AAY23565 standard; protein: 194 AA.  
DE Human EST encoded protein SEQ ID NO: 1090.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 86.1%; Score 949; DB 4; Length 184;

Best Local Similarity 99.5%; Pred. No. 6.3e-97;  
RESULT 320  
ID AD007065 standard; protein: 217 AA.  
DE Human protein modification and maintenance molecule 26 (PMM-26).  
PN WO2004033636-A2.  
PD 22-APR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 80.3%; Score 885; DB 8; Length 217;  
Best Local Similarity 100.0%; Pred. No. 1.1e-89;  
RESULT 321  
ID AAY11999 standard; protein: 136 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 312.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GSEST ) GENSET.  
Query Match 63.0%; Score 694; DB 2; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.1e-68;  
RESULT 322  
ID AAY36576 standard; protein: 176 AA.  
DE Fragment of human secreted protein encoded by gene 42.  
PN WO9931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 60.2%; Score 663; DB 2; Length 176;  
Best Local Similarity 96.3%; Pred. No. 4.3e-65;  
RESULT 323  
ID ADA11746 standard; protein: 176 AA.  
DE Human novel secreted protein associated polypeptide #16.  
PN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 60.2%; Score 663; DB 6; Length 176;  
Best Local Similarity 96.3%; Pred. No. 4.3e-65;  
RESULT 324  
ID ADN42960 standard; protein: 119 AA.  
DE Human secreted protein SECP-21.  
PN WO2004037987-A2.  
PD 06-MAY-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 43.5%; Score 479.5; DB 8; Length 119;  
Best Local Similarity 50.0%; Pred. No. 6.4e-45;  
RESULT 325  
ID ADA57438 standard; protein: 104 AA.  
DE Human secreted protein #269.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.7%; Score 415; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 8e-38;  
RESULT 326  
ID ADA41317 standard; protein: 104 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.7%; Score 415; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 8e-38;  
RESULT 327  
ID ADD38041 standard; protein: 104 AA.  
DE Human secreted protein #224.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.7%; Score 415; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 8e-38;  
RESULT 328  
ID AAY36265 standard; protein: 105 AA.  
DE Human secreted protein encoded by gene 42.  
PN WO9931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.7%; Score 415; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 8.1e-38;

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RESULT 329
ID ADA11718 standard; protein; 105 AA.
DE Human novel secreted protein, SEQ ID NO 246.
PN US2003055236-A1.
ID 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 37.7%; Score 415; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.1e-38;
RESULT 330
ID ABM65140 standard; protein; 768 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:5389.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 34.1%; Score 376; DB 8; Length 768;
Best Local Similarity 47.9%; Pred. No. 2.8e-32;
RESULT 331
ID AAY64562 standard; protein; 805 AA.
DE A human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO20001889-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 3; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 332
ID AAY67310 standard; protein; 805 AA.
DE Human MPROT15 amino acid sequence #1.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMK-) SMITHKLINE BEECHAM PLC.
Query Match 34.1%; Score 376; DB 3; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 333
ID AAB48095 standard; protein; 805 AA.
DE Human Zace2 protein.
PN WO200070033-A1.
PD 23-NOV-2000.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 334
ID AAY72667 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2).
PN US6194556-B1.
PD 27-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 335
ID AAE20353 standard; protein; 805 AA.
DE Human ACE-2 full-length protein.
PN WO200212471-A2.
PD 14-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 336
ID ABG77011 standard; protein; 805 AA.
DE Human angiotensin converting enzyme 2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
PA (TSUC-) TSUCHIHASHI Z.
PA (HUI/) HUI L.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 337
ID ABG77023 standard; protein; 805 AA.
DE Human angiotensin converting enzyme 2 variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
PA (TSUC-) TSUCHIHASHI Z.
PA (HUI/) HUI L.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 338
ID AAY9701 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO200239997-A2.
PD 23-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 339
ID ABU07731 standard; protein; 805 AA.
DE Human zinc metalloproteinase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 34.1%; Score 376; DB 6; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 340
ID ADA03344 standard; protein; 805 AA.
DE Human angiotensin converting enzyme 2-like protein.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.1%; Score 376; DB 6; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 341
ID ABR56712 standard; protein; 805 AA.
DE Human ACE-2 protein SEQ ID NO:142.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.1%; Score 376; DB 6; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 342
ID ADC38728 standard; protein; 805 AA.
DE Human secreted protein #41.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GENY-) GENETICS INST INC.
Query Match 34.1%; Score 376; DB 7; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 343
ID ADL95395 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2).
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 7; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 344
ID ADL95494 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2) N720D.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 7; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 345
ID ADH51357 standard; protein; 805 AA.
DE Human angiotensin-converting enzyme homologue ACE2.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Query Match 34.1%; Score 376; DB 8; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 346
ID ADO55144 standard; protein; 805 AA.
DE Protein #46 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
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Query Match 34.1%; Score 376; DB 8; Length 805;  
Best Local Similarity 47.9%; Pred. No. 3e-32;  
RESULT 347  
ID ADA03340 standard; protein; 711 AA.  
DE Human angiotensin converting enzyme 2 protein.  
PN WO200298448-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.8%; Score 362; DB 6; Length 711;  
Best Local Similarity 48.8%; Pred. No. 9.2e-31;  
RESULT 348  
ID AAB48097 standard; protein; 805 AA.  
DE Mouse Zace2-5 protein.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 32.8%; Score 361; DB 4; Length 805;  
Best Local Similarity 40.9%; Pred. No. 1.4e-30;  
RESULT 349  
ID AAB48098 standard; protein; 805 AA.  
DE Mouse Zace2-10 protein.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 32.8%; Score 361; DB 4; Length 805;  
Best Local Similarity 40.9%; Pred. No. 1.4e-30;  
RESULT 350  
ID AAB07733 standard; protein; 805 AA.  
DE Mouse zinc metalloproteinase mZace-5.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 32.8%; Score 361; DB 6; Length 805;  
Best Local Similarity 40.9%; Pred. No. 1.4e-30;  
RESULT 351  
ID ABOU7734 standard; protein; 805 AA.  
DE Mouse zinc metalloproteinase mZace-10.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 32.8%; Score 361; DB 6; Length 805;  
Best Local Similarity 40.9%; Pred. No. 1.4e-30;  
RESULT 352  
ID AAU09092 standard; protein; 711 AA.  
DE Novel human protein NHP #1.  
PN WO200174896-A1.  
PD 11-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.6%; Score 359; DB 4; Length 711;  
Best Local Similarity 47.2%; Pred. No. 2e-30;  
RESULT 353  
ID ABR56709 standard; protein; 711 AA.  
DE Human ACE-2 protein SEQ ID NO.138.  
PN WO200298906-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 32.6%; Score 359; DB 6; Length 711;  
Best Local Similarity 47.2%; Pred. No. 2e-30;  
RESULT 354  
ID ABR40295 standard; peptide; 64 AA.  
DE Peptide #7801 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 355  
ID AAM33978 standard; protein; 64 AA.  
DE Peptide #8015 encoded by probe for measuring placental gene expression.  
PN WO300157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 4; Length 64;

Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 356  
ID ABR24701 standard; protein; 64 AA.  
DE Protein #6700 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 357  
ID AAM73792 standard; protein; 64 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO. 34098.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 358  
ID AAM61088 standard; protein; 64 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO. 33193.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 359  
ID ABR55539 standard; peptide; 64 AA.  
DE Human liver peptide, SEQ ID NO 34187.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 360  
ID ABR43678 standard; peptide; 64 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33343.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 29.9%; Score 330; DB 5; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
RESULT 361  
ID ABR85139 standard; protein; 771 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO.5388.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 27.0%; Score 297; DB 8; Length 771;  
Best Local Similarity 41.2%; Pred. No. 1.8e-23;  
RESULT 362  
ID ADA03342 standard; protein; 681 AA.  
DE Human angiotensin converting enzyme 2 extracellular domain.  
PN WO200298448-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 26.2%; Score 289; DB 6; Length 681;  
Best Local Similarity 48.1%; Pred. No. 1.1e-22;  
RESULT 363  
ID ABR56711 standard; protein; 681 AA.  
DE Human ACE-2 extracellular domain SEQ ID NO.140.  
PN WO200298906-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 26.2%; Score 289; DB 6; Length 681;  
Best Local Similarity 48.1%; Pred. No. 1.1e-22;  
RESULT 364  
ID AAT36579 standard; protein; 24 AA.  
DE Fragment of human secreted protein encoded by gene 42.  
PN WO9931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.1%; Score 133; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;



RESULT 365  
ID ADA11749 standard; protein; 24 AA.  
DE Human novel secreted protein associated polypeptide #19.  
FN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.1%; Score 133; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
RESULT 366  
ID AAY36578 standard; protein; 23 AA.  
DE Fragment of human secreted protein encoded by gene 42.  
FN WO9931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.6%; Score 117; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 367  
ID ADA11748 standard; protein; 23 AA.  
DE Human novel secreted protein associated polypeptide #18.  
FN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.6%; Score 117; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
RESULT 368  
ID ABB70857 standard; protein; 929 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39363.  
FN WO20011042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 8.5%; Score 93.5; DB 4; Length 929;  
Best Local Similarity 28.8%; Pred. No. 0.99;  
RESULT 369  
ID ABB72288 standard; protein; 545 AA.  
DE Murine protein isolated from skin cells SEQ ID NO: 500.  
FN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 8.3%; Score 91.5; DB 5; Length 545;  
Best Local Similarity 20.4%; Pred. No. 0.79;  
RESULT 370  
ID ABB72300 standard; protein; 688 AA.  
DE Rat protein isolated from skin cells SEQ ID NO: 624.  
FN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 8.3%; Score 91.5; DB 5; Length 688;  
Best Local Similarity 20.4%; Pred. No. 1.1;  
RESULT 371  
ID AAB50087 standard; protein; 1188 AA.  
DE Murine A259.  
FN WO200073339-A1.  
PD 07-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 91.5; DB 4; Length 1188;  
Best Local Similarity 20.5%; Pred. No. 2.3;  
RESULT 372  
ID AAU10552 standard; protein; 1188 AA.  
DE Murine A259 polypeptide.  
FN WO200181414-A2.  
PD 01-NOV-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 91.5; DB 5; Length 1188;  
Best Local Similarity 20.5%; Pred. No. 2.3;  
RESULT 373  
ID AAY6577 standard; protein; 25 AA.  
DE Fragment of human secreted protein encoded by gene 42.  
FN WO9931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.2%; Score 90; DB 2; Length 25;  
Best Local Similarity 78.3%; Pred. No. 0.016;  
RESULT 374

ID ADA11747 standard; protein; 25 AA.  
DE Human novel secreted protein associated polypeptide #17.  
FN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.2%; Score 90; DB 6; Length 25;  
Best Local Similarity 78.3%; Pred. No. 0.016;  
RESULT 375  
ID AAW25639 standard; protein; 799 AA.  
DE Rat full length cadherin-8.  
FN US5646250-A.  
PD 08-JUL-1997.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 8.2%; Score 90; DB 2; Length 799;  
Best Local Similarity 21.4%; Pred. No. 2;  
RESULT 376  
ID AAW13126 standard; protein; 799 AA.  
DE Full length rat cadherin-8.  
FN US5597725-A.  
PD 28-JAN-1997.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 8.2%; Score 90; DB 2; Length 799;  
Best Local Similarity 21.4%; Pred. No. 2;  
RESULT 377  
ID AAW25635 standard; protein; 793 AA.  
DE Human cadherin-8.  
FN US5646250-A.  
PD 08-JUL-1997.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 8.1%; Score 89.5; DB 2; Length 793;  
Best Local Similarity 20.6%; Pred. No. 2.2;  
RESULT 378  
ID AAW13132 standard; protein; 793 AA.  
DE Full length human cadherin-8.  
FN US5597725-A.  
PD 28-JAN-1997.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 8.1%; Score 89.5; DB 2; Length 793;  
Best Local Similarity 20.6%; Pred. No. 2.2;  
RESULT 379  
ID AAM39241 standard; protein; 1035 AA.  
DE Human polypeptide SEQ ID NO 2386.  
FN WO200153312-A1.  
PD 26-JUN-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.1%; Score 89.5; DB 4; Length 1035;  
Best Local Similarity 20.2%; Pred. No. 3.2;  
RESULT 380  
ID AAM41027 standard; protein; 1044 AA.  
DE Human polypeptide SEQ ID NO 5958.  
FN WO200153312-A1.  
PD 26-JUN-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.1%; Score 89.5; DB 4; Length 1044;  
Best Local Similarity 20.2%; Pred. No. 3.3;  
RESULT 381  
ID AAE20902 standard; protein; 1063 AA.  
DE Human INTG-1 protein.  
FN WO200212339-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 8.1%; Score 89.5; DB 5; Length 1063;  
Best Local Similarity 20.2%; Pred. No. 3.3;  
RESULT 382  
ID AAB19350 standard; protein; 1063 AA.  
DE NOVX related protein SEQ ID NO 66.  
FN WO200299062-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 89.5; DB 6; Length 1063;  
Best Local Similarity 20.2%; Pred. No. 3.3;  
RESULT 383  
ID ADO41700 standard; protein; 1063 AA.

PA	(KEKU/) KEKUDA R.			
PA	(PATT/) PATTURAJAN M.			
PA	(SPYT/) SPYTEK K A.			
PA	(LEIT/) LEITE M W.			
PA	(RAST/) RASTELLI L.			
PA	(MAD/) MACDOUGALL J R.			
PA	(TAUP/) TAUPIER R J.			
PA	(GUXO/) GUXO X S.			
PA	(MILL/) MILLER C E.			
PA	(SHEN/) SHENOY S G.			
PA	(HJAL/) HJALT T.			
PA	(VOSS/) VOSS E Z.			
PA	(BOLD/) BOLDOG F L.			
PA	(MALY/) MALYANKAR U M.			
PA	(PADI/) PADIGARU M.			
PA	(JTWI/) JT W.			
PA	(SMIT/) SMITHSON G.			
PA	(EDIN/) EDINGER S R.			
PA	(MILT/) MILETT I.			
PA	(ELBE/) ELBERMAN K.			
Query Match		8.0%;	Score 88.5; DB 8;	Length 1063;
Best Local Similarity		20.2%;	Pred. No. 4.3;	
RESULT 388				
ID	AAB50929 standard; protein; 1188 AA.			
DE	Amino acid sequence of a human alphaII integrin chain.			
PN	WO200075187-A1.			
PD	14-DEC-2000.			
PA	(ACTI-) ACTIVE BIOTECH AB.			
Query Match		8.0%;	Score 88.5; DB 4;	Length 1188;
Best Local Similarity		22.6%;	Pred. No. 5.1;	
RESULT 389				
ID	ABR33337 standard; peptide; 15 AA.			
DE	Human cancer-related protein 156P5C12 HLA peptide #1690.			
PN	WO200283921-A2.			
PD	24-OCT-2002.			
PA	(AGEN-) AGENSYS INC.			
Query Match		8.0%;	Score 88; DB 6;	Length 15;
Best Local Similarity		100.0%;	Pred. No. 0.013;	
RESULT 390				
ID	ABR33285 standard; peptide; 15 AA.			
DE	Human cancer-related protein 156P5C12 HLA peptide #1638.			
PN	WO200283921-A2.			
PD	24-OCT-2002..			
PA	(AGEN-) AGENSYS INC.			
Query Match		8.0%;	Score 88; DB 6;	Length 15;
Best Local Similarity		100.0%;	Pred. No. 0.013;	
RESULT 391				
ID	ABU79109 standard; protein; 365 AA.			
DE	CD4 protein.			
PN	US2002177551-A1.			
PD	28-NOV-2002.			
PA	(TERM/) TERMAN D S.			
Query Match		8.0%;	Score 88; DB 6;	Length 365;
Best Local Similarity		21.6%;	Pred. No. 1.1;	
RESULT 392				
ID	ADF43353 standard; protein; 365 AA.			
DE	CD4 receptor polypeptide seq id 73.			
PN	US2003157113-A1.			
PD	21-AUG-2003.			
PA	(TERM/) TERMAN D S.			
Query Match		8.0%;	Score 88; DB 7;	Length 365;
Best Local Similarity		21.6%;	Pred. No. 1.1;	
RESULT 393				
ID	ABB6068 standard; protein; 968 AA.			
DE	Drosophila melanogaster polypeptide SEQ ID NO 6996.			
PN	WO20011042-A2.			
PD	27-SEP-2001.			
PA	(PEKE ) PE CORP NY.			
Query Match		7.8%;	Score 86.5; DB 4;	Length 968;
Best Local Similarity		19.1%;	Pred. No. 6.3;	
RESULT 394				
ID	ABR33291 standard; peptide; 15 AA.			
DE	Human cancer-related protein 156P5C12 HVA peptide #1644.			

PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.8%; Score 86; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
RESULT 395  
ID ABR33284 atandard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1637.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.8%; Score 86; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
RESULT 396  
ID ABR33406 atandard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1759.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.8%; Score 86; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
RESULT 397  
ID ABR3375 atandard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1728.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.8%; Score 86; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
RESULT 398  
ID ABR3334 atandard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1677.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.8%; Score 86; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
RESULT 399  
ID ABR3382 atandard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1735.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.8%; Score 86; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
RESULT 400  
ID ABB81033 atandard; protein; 364 AA.  
DE Rat glycoprotein CD44 polypeptide.  
PN WO200238794-A2.  
PD 16-MAY-2002.  
PA (BCHM-) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 7.8%; Score 86; DB 5; Length 364;  
Best Local Similarity 20.7%; Pred. No. 1.8;  
RESULT 401  
ID AAR14768 atandard; protein; 503 AA.  
DE Metastasis-specific variant of CD44 glycoprotein.  
PN DE4014510-A.  
PD 14-NOV-1991.  
PA (GSSL-) KERNFORSCHUNGSZENT KARLSRUHE.  
PA (UYKA-) UNIV KARLSRUHE.  
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.  
Query Match 7.8%; Score 86; DB 2; Length 503;  
Best Local Similarity 20.7%; Pred. No. 2.9;  
RESULT 402  
ID ADB57911 atandard; protein; 503 AA.  
DE Rat Protein P26051, SEQ ID NO 3777.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GHO-) GEN HOSPITAL CORP.  
PA (PARB-) BAYER AG.  
Query Match 7.8%; Score 86; DB 7; Length 503;  
Best Local Similarity 20.7%; Pred. No. 2.9;

RESULT 403  
ID ABP77872 atandard; protein; 468 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 2274.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.8%; Score 85.5; DB 6; Length 468;  
Best Local Similarity 24.1%; Pred. No. 3;  
RESULT 404  
ID AAU31438 atandard; protein; 543 AA.  
DE Novel human secreted protein #1929.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 85.5; DB 4; Length 543;  
Best Local Similarity 19.8%; Pred. No. 3.6;  
RESULT 405  
ID ABB92524 atandard; protein; 667 AA.  
DE Hericidially active polypeptide SEQ ID NO 1735.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match 7.8%; Score 85.5; DB 5; Length 667;  
Best Local Similarity 21.6%; Pred. No. 4.9;  
RESULT 406  
ID AAB95836 atandard; protein; 1148 AA.  
DE Human protein sequence SEQ ID NO:18865.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.8%; Score 85.5; DB 4; Length 1148;  
Best Local Similarity 21.4%; Pred. No. 10;  
RESULT 407  
ID ABB50283 atandard; protein; 1148 AA.  
DE HOST-1 ovarian tumour marker protein, SEQ ID NO:56.  
PN WO200175177-A2.  
PD 11-OCT-2001.  
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 7.8%; Score 85.5; DB 4; Length 1148;  
Best Local Similarity 21.4%; Pred. No. 10;  
RESULT 408  
ID ABG96380 atandard; protein; 1148 AA.  
DE Human ovarian cancer marker M461.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 85.5; DB 5; Length 1148;  
Best Local Similarity 21.4%; Pred. No. 10;  
RESULT 409  
ID ABP30964 atandard; protein; 1148 AA.  
DE Truncated version protein with sequence homology to 0772P.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 85.5; DB 5; Length 1148;  
Best Local Similarity 21.4%; Pred. No. 10;  
RESULT 410  
ID ABP30969 atandard; protein; 1148 AA.  
DE Clone FLJ14303.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 85.5; DB 5; Length 1148;  
Best Local Similarity 21.4%; Pred. No. 10;  
RESULT 411  
ID ADA08632 atandard; protein; 1148 AA.  
DE Human O772P partial protein #2.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.

PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1148;  
Pred. No. 10;  
RESULT 412  
ID ADA08611 standard; protein; 1148 AA.  
DE Human O772P homology protein #1.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1148;  
Pred. No. 10;  
RESULT 413  
ID ADF08954 standard; protein; 1148 AA.  
DE Secreted ovarian carcinoma antigen seqid 458.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1148;  
Pred. No. 10;  
RESULT 414  
ID ADF08975 standard; protein; 1148 AA.  
DE Secreted ovarian carcinoma antigen seqid 479.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1148;  
Pred. No. 10;  
RESULT 415  
ID ADG46241 standard; protein; 1148 AA.  
DE Human ovarian carcinoma polypeptide #47.  
PN US2003165504-A1.  
PD 04-SEP-2003.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1148;  
Pred. No. 10;  
RESULT 416  
ID ADM30754 standard; protein; 1148 AA.  
DE Human cancer linked protein referred to as 225250 seqid 2.  
PN WO2003075854-A2.  
PD 18-SEP-2003.  
PA (AVAL-) AVALON PHARM.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1148;  
Pred. No. 10;  
RESULT 417  
ID ADQ29705 standard; protein; 1148 AA.  
DE Human colorectal cancer-associated protein #60.  
PN EPI439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 8; Length 1148;  
Pred. No. 10;  
RESULT 418  
ID ABR30965 standard; protein; 1156 AA.  
DE Protein with sequence homology to 0772P.  
PN WO200206317-A2.

PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 5; Length 1156;  
Pred. No. 10;  
RESULT 419  
ID ADA08612 standard; protein; 1156 AA.  
DE Human O772P homology protein #2.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1156;  
Pred. No. 10;  
RESULT 420  
ID ADF08955 standard; protein; 1156 AA.  
DE Secreted ovarian carcinoma antigen seqid 459.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1156;  
Pred. No. 10;  
RESULT 421  
ID ADG46242 standard; protein; 1156 AA.  
DE Human ovarian carcinoma polypeptide #48.  
PN US2003165504-A1.  
PD 04-SEP-2003.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 7; Length 1156;  
Pred. No. 10;  
RESULT 422  
ID ABR58656 standard; protein; 1482 AA.  
DE Human cancer related protein SEQ ID NO:313.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 6; Length 1482;  
Pred. No. 15;  
RESULT 423  
ID ABP69627 standard; protein; 1497 AA.  
DE Human polypeptide SEQ ID NO 1674.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 5; Length 1497;  
Pred. No. 15;  
RESULT 424  
ID AAE34700 standard; protein; 1889 AA.  
DE Protein encoded by B4 DNA clone (CA125) .  
PN WO200292836-A2.  
PD 21-NOV-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match  
Best Local Similarity 7.8%; Score 85.5; DB 6; Length 1889;  
Pred. No. 21;  
RESULT 425  
ID ABR33304 standard; peptide; 15 AA.  
DE Human cancer-related protein 156F5C12 HLA peptide #1657.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 7.7%; Score 85; DB 6; Length 15;  
Pred. No. 0.027;  
RESULT 426  
ID ABR33390 standard; peptide; 15 AA.

DE Human cancer-related protein 156P5C12 HLA peptide #1743.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 427  
ID ABR33438 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1791.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 428  
ID ABR33367 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1720.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 429  
ID ABR33395 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1748.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 430  
ID ABR33321 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1674.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 431  
ID ABR33400 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1753.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 432  
ID ABR33317 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1670.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 433  
ID ABR33316 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1354.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 434  
ID ABR33087 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1305.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 435  
ID ABR33108 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1326.

PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 436  
ID ABR33325 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1678.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 6; Length 15;  
RESULT 437  
ID ADL16195 standard; protein; 1337 AA.  
DE Human protein tyrosine phosphatase #14.  
PN WO2003068984-A2.  
PD 21-AUG-2003.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PA (CBPT-) CBPT INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Score 85; DB 7; Length 1337;  
RESULT 438  
ID AAY75167 standard; protein; 468 AA.  
DE Neisseria meningitidis ORF 585 protein sequence SEQ ID NO:1808.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 23.7%; Pred. No. 3.8;  
Score 84.5; DB 3; Length 468;  
RESULT 439  
ID AAU14467 standard; protein; 1188 AA.  
DE Human novel protein #338.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 22.5%; Pred. No. 14;  
Score 84.5; DB 4; Length 1188;  
RESULT 440  
ID AAU14231 standard; protein; 1188 AA.  
DE Human novel protein #102.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 22.5%; Pred. No. 14;  
Score 84.5; DB 4; Length 1188;  
RESULT 441  
ID AAB50085 standard; protein; 1188 AA.  
DE Human A259.  
PN WO200073339-A1.  
PD 07-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 22.5%; Pred. No. 14;  
Score 84.5; DB 4; Length 1188;  
RESULT 442  
ID AAU10551 standard; protein; 1188 AA.  
DE Human A259 polypeptide.  
PN WO200181414-A2.  
PD 01-NOV-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 22.5%; Pred. No. 14;  
Score 84.5; DB 5; Length 1188;  
RESULT 443  
ID ADE09956 standard; protein; 1188 AA.  
DE Novel protein-related contig polypeptide sequence #544.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 22.5%; Pred. No. 14;  
Score 84.5; DB 7; Length 1188;  
RESULT 444  
ID ABR33383 standard; peptide; 15 AA.

DE Human cancer-related protein 156P5C12 HLA peptide #1736.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.6%; Score 84; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
RESULT 445  
ID ABR33116 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1334.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.6%; Score 84; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
RESULT 446  
ID ABR33302 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1655.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.6%; Score 84; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
RESULT 447  
ID ABR33452 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1805.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.6%; Score 84; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
RESULT 448  
ID ABR33126 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1344.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.6%; Score 84; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
RESULT 449  
ID ABR33314 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1667.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.6%; Score 84; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
RESULT 450  
ID ABR85203 standard; protein: 1337 AA.  
DE HUDEF-1.  
PN WO9530008-A1.  
PD 09-NOV-1995.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 7.6%; Score 83.5; DB 2; Length 1337;  
Best Local Similarity 26.4%; Pred. No. 21;  
RESULT 451  
ID ADL16193 standard; protein: 1337 AA.  
DE Human protein tyrosine phosphatase #13.  
PN WO2003068984-A2.  
PD 21-AUG-2003.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 7.6%; Score 83.5; DB 7; Length 1337;  
Best Local Similarity 26.4%; Pred. No. 21;  
RESULT 452  
ID ADP74603 standard; protein: 1337 AA.  
DE Amino acid sequence of human DEP-1.  
PN WO2004048549-A2.  
PD 10-JUN-2004.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 7.6%; Score 83.5; DB 8; Length 1337;  
Best Local Similarity 26.4%; Pred. No. 21;  
RESULT 453  
ID ABR33125 standard; peptide: 15 AA.

DE Human cancer-related protein 156P1D4 HLA peptide #1343.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 454  
ID ABR33398 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1751.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 455  
ID ABR33351 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1704.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 456  
ID ABR33297 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1650.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 457  
ID ABR33427 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1780.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 458  
ID ABR33115 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1333.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 459  
ID ABR33336 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1689.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 460  
ID ABR33363 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1716.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 461  
ID ABR33113 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1331.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.5%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
RESULT 462  
ID AAY75165 standard; protein: 231 AA.  
DE Neisseria gonorrhoeae ORF 585 protein sequence SEQ ID NO:1804.

PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 7.5%; Score 82.5; DB 3; Length 231;  
Best Local Similarity 24.1%; Pred. No. 2.4;  
RESULT 463  
ID ADH8063 standard; protein; 529 AA.  
DE Enterococcus faecalis polypeptide #2543.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L. A.  
PA (BUSH/) BUSH D.  
Query Match 7.5%; Score 82.5; DB 7; Length 529;  
Best Local Similarity 24.7%; Pred. No. 7.6;  
RESULT 464  
ID ADS94303 standard; protein; 809 AA.  
DE CA 125/O772P 3-repeat TM amino acid sequence SEQ ID NO:2.  
PN WO2004035537-A2.  
PD 29-APR-2004.  
PA (EURO-) EUROCELLTQUE SA.  
Query Match 7.5%; Score 82.5; DB 8; Length 809;  
Best Local Similarity 20.3%; Pred. No. 14;  
RESULT 465  
ID ABR3333 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1676.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 466  
ID ABR33397 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1750.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 467  
ID ABR33084 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1302.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 468  
ID ABR33296 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1649.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 469  
ID ABR33290 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1643.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 470  
ID ABR3333 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1666.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 471  
ID ABR33391 standard; peptide; 15 AA.

DE Human cancer-related protein 156P5C12 HLA peptide #1744.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 472  
ID ABR33109 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1327.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 473  
ID ABR33373 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1726.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 474  
ID ABR33436 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1789.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 475  
ID ABR33097 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1315.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 476  
ID ABR33420 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1773.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 82; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
RESULT 477  
ID ABR58365 standard; protein; 1120 AA.  
DE Human NOV2B.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.4%; Score 82; DB 6; Length 1120;  
Best Local Similarity 21.4%; Pred. No. 25;  
RESULT 478  
ID AAB35582 standard; protein; 1189 AA.  
DE ITGA11 protein encoded by human secreted protein gene #7.  
PN WO200029435-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.4%; Score 82; DB 3; Length 1189;  
Best Local Similarity 21.4%; Pred. No. 27;  
RESULT 479  
ID ABR58364 standard; protein; 1189 AA.  
DE Human NOV2a.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.4%; Score 82; DB 6; Length 1189;  
Best Local Similarity 21.4%; Pred. No. 27;  
RESULT 480  
ID ADA27054 standard; protein; 1189 AA.  
DE Human novel secreted protein from cDNA HONBY69 #1.

PN US2003055231-A1.  
PD 20-MAR-2003.  
PA (NITU//) NIT J.  
PA (YOUN//) YOUNG P E.  
PA (KENN//) KENNY J J.  
PA (OLSE//) OLSEN H S.  
PA (MOOR//) MOORE P A.  
PA (WEIY//) WEI Y.  
PA (GREE//) GREENE J M.  
PA (RUBE//) RUBEN S M.  
PA (LITD//) LIT D.  
PA (CROC//) CROCKER P R.  
Query Match  
Best Local Similarity 7.4%; Score 82; DB 6; Length 1189;  
21.4%; Pred. No. 27;  
RESULT 481  
ID ADE63570 standard; protein; 1189 AA.  
DE Human Protein Q9UKX5, SEQ ID NO 9514.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 7.4%; Score 82; DB 7; Length 1189;  
21.4%; Pred. No. 27;  
RESULT 482  
ID ADE86584 standard; protein; 1189 AA.  
DE Novel human secreted protein #7.  
PN US2003129685-A1.  
PD 10-JUN-2003.  
PA (NITU//) NIT J.  
PA (YOUN//) YOUNG P E.  
PA (KENN//) KENNY J J.  
PA (OLSE//) OLSEN H S.  
PA (MOOR//) MOORE P A.  
PA (WEIY//) WEI Y.  
PA (GREE//) GREENE J M.  
PA (RUBE//) RUBEN S M.  
Query Match  
Best Local Similarity 7.4%; Score 82; DB 8; Length 1189;  
21.4%; Pred. No. 27;  
RESULT 483  
ID ADQ19968 standard; protein; 1189 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2788.  
PN WO2004048538-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 7.4%; Score 82; DB 8; Length 1189;  
21.4%; Pred. No. 27;  
RESULT 484  
ID ADL16200 standard; protein; 1216 AA.  
DE Rat protein tyrosine phosphatase #4.  
PN WO2003068984-A2.  
PD 21-AUG-2003.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PA (CEPT-) CEPTAR INC.  
Query Match  
Best Local Similarity 7.4%; Score 82; DB 7; Length 1216;  
26.7%; Pred. No. 28;  
RESULT 485  
ID ABP68575 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NC5M) Protein SEQ ID NO:268.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 5; Length 302;  
23.9%; Pred. No. 4.5;  
RESULT 486  
ID ADM18903 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:268.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 8; Length 302;  
23.9%; Pred. No. 4.5;  
RESULT 487  
ID ABW69195 standard; protein; 364 AA.

DE Photorhabdus luminescens protein sequence #2292.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 6; Length 364;  
25.0%; Pred. No. 5.8;  
RESULT 488  
ID AAU76335 standard; peptide; 1048 AA.  
DE Human anti-dual integrin protein #1.  
PN WO200212501-A2.  
PD 14-FEB-2002.  
PA (CENZ ) CENTOCOR INC.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 5; Length 1048;  
23.7%; Pred. No. 25;  
RESULT 489  
ID ABU03549 standard; protein; 1048 AA.  
DE Angiogenesis-associated human protein sequence #94.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 6; Length 1048;  
23.7%; Pred. No. 25;  
RESULT 490  
ID AAO27098 standard; protein; 1048 AA.  
DE Human integrin alpha-V precursor (CD51).  
PN WO2003010190-A2.  
PD 06-FEB-2003.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
PA (BIOA-) BIOACTA LTD.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 6; Length 1048;  
23.7%; Pred. No. 25;  
RESULT 491  
ID ABB82767 standard; protein; 1048 AA.  
DE Human alphavbeta3 integrin alphav subunit sequence.  
PN WO200287505-A2.  
PD 07-NOV-2002.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 6; Length 1048;  
23.7%; Pred. No. 25;  
RESULT 492  
ID ADD48691 standard; protein; 1048 AA.  
DE Human Protein NP\_002201, SEQ ID NO 14602.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 7; Length 1048;  
23.7%; Pred. No. 25;  
RESULT 493  
ID ABG18695 standard; protein; 1061 AA.  
DE Novel human diagnostic protein #18866.  
PN WO200175057-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.4%; Score 81.5; DB 4; Length 1061;  
23.7%; Pred. No. 26;  
RESULT 494  
ID ABR33098 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1316.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 7.4%; Score 81; DB 6; Length 15;  
100.0%; Pred. No. 0.076;  
RESULT 495  
ID ABR33369 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1722.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 7.4%; Score 81; DB 6; Length 15;



Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 496  
ID ABR3370 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1723.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 497  
ID ABR33419 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1772.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 498  
ID ABR33341 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1694.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 499  
ID ABR33309 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1662.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 500  
ID ABR33384 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1737.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 501  
ID ABR33107 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1325.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 502  
ID ABR33371 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1724.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 503  
ID ABR33404 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1757.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 504  
ID ABR33408 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1761.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;

RESULT 505  
ID ABR33428 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1781.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 506  
ID ABR33387 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1740.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 507  
ID ABR33443 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1796.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 508  
ID ABR33447 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1800.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 509  
ID ABR33300 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1653.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 510  
ID ABR33083 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1301.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.4%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
RESULT 511  
ID ABUS4859 standard; protein; 284 AA.  
DE Human CA125 carboxy terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.3%; Score 80.5; DB 6; Length 284;  
Best Local Similarity 20.8%; Pred. No. 5.3;  
RESULT 512  
ID AAB12623 standard; protein; 438 AA.  
DE Human gene 1 encoded secreted protein HRP230.  
PN WO200170804-A1.  
PD 27-SEP-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.3%; Score 80.5; DB 4; Length 438;  
Best Local Similarity 20.8%; Pred. No. 9.7;  
RESULT 513  
ID ABP30973 standard; protein; 438 AA.  
DE Partial protein sequence of clone 0772p partial cDNA sequence 4.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIYA CORP.  
Query Match 7.3%; Score 80.5; DB 5; Length 438;  
Best Local Similarity 20.8%; Pred. No. 9.7;  
RESULT 514

ID ADA08636 standard; protein; 438 AA.  
DE Human O772P partial protein #6.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match 7.3%; Score 80.5; DB 7; Length 438;  
Best Local Similarity 20.8%; Pred. No. 9.7;  
RESULT 515  
ID ADF08979 standard; protein; 438 AA.  
DE Secreted ovarian carcinoma antigen seqid 483.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIYA CORP.  
Query Match 7.3%; Score 80.5; DB 7; Length 438;  
Best Local Similarity 20.8%; Pred. No. 9.7;  
RESULT 516  
ID ABUS4709 standard; protein; 439 AA.  
DE Human CA125 protein carboxy terminus.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.3%; Score 80.5; DB 6; Length 439;  
Best Local Similarity 20.8%; Pred. No. 9.7;  
RESULT 517  
ID AAE12634 standard; protein; 526 AA.  
DE Human gene 1 encoded secreted protein fragment, SEQ ID NO: 30.  
PN WO200170804-A1.  
PD 27-SEP-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.3%; Score 80.5; DB 4; Length 526;  
Best Local Similarity 20.8%; Pred. No. 13;  
RESULT 518  
ID ABB93901 standard; protein; 675 AA.  
DE Heblcidentally active polypeptide SEQ ID NO 3112.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match 7.3%; Score 80.5; DB 5; Length 675;  
Best Local Similarity 26.6%; Pred. No. 18;  
RESULT 519  
ID ABUS4692 standard; protein; 1148 AA.  
DE Human CA125 protein from CDNA AKO24365.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.3%; Score 80.5; DB 6; Length 1148;  
Best Local Similarity 20.8%; Pred. No. 37;  
RESULT 520  
ID ABU00145 standard; protein; 1148 AA.  
DE Human novel polypeptide #238.  
PN WO200274961-A1.  
PD 26-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.3%; Score 80.5; DB 6; Length 1148;  
Best Local Similarity 20.8%; Pred. No. 37;  
RESULT 521  
ID ADH41326 standard; protein; 1148 AA.  
DE Human ovarian specific gene (OSG) protein.  
PN US2003096238-A1.  
PD 22-MAY-2003.  
PA (SALC/) SALCEDA S.  
PA (CAFF/) CAFFERKEY R.  
Query Match 7.3%; Score 80.5; DB 8; Length 1148;

Best Local Similarity 20.8%; Pred. No. 37;  
RESULT 522  
ID ADR10190 standard; protein; 1307 AA.  
DE Human protein useful for treating neurological disease Seq 3696.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.3%; Score 80.5; DB 8; Length 1307;  
Best Local Similarity 20.8%; Pred. No. 45;  
RESULT 523  
ID ABUS4693 standard; protein; 2248 AA.  
DE Human CA125 protein with 13 repeats and the carboxy terminus.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.3%; Score 80.5; DB 6; Length 2248;  
Best Local Similarity 20.8%; Pred. No. 96;  
RESULT 524  
ID ABUS4721 standard; protein; 11721 AA.  
DE Human CA125 full length protein sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.3%; Score 80.5; DB 6; Length 11721;  
Best Local Similarity 20.8%; Pred. No. 9.6e+02;  
RESULT 525  
ID ADR72871 standard; protein; 22152 AA.  
DE Human ovarian cancer-related tumour marker CA125 protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN-) MOUNT SINAI HOSPITAL.  
Query Match 7.3%; Score 80.5; DB 8; Length 22152;  
Best Local Similarity 20.8%; Pred. No. 2.3e+03;  
RESULT 526  
ID ADP84155 standard; protein; 22157 AA.  
DE Human CA125 protein sequence SeqID 5.  
PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.3%; Score 80.5; DB 8; Length 22157;  
Best Local Similarity 20.8%; Pred. No. 2.3e+03;  
RESULT 527  
ID ABR33122 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1340.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.3%; Score 80; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.098;  
RESULT 528  
ID ABR33172 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1725.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.3%; Score 80; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.098;  
RESULT 529  
ID ABR33434 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1787.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.3%; Score 80; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.098;  
RESULT 530  
ID ABR33435 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1788.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.3%; Score 80; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.098;

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RESULT 531
ID ABR33310 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1663.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.3%; Score 80; DB 6; Length 15;
Pred. No. 0.098;
RESULT 532
ID ABR33414 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1767.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.3%; Score 80; DB 6; Length 15;
Pred. No. 0.098;
RESULT 533
ID ABR33132 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1350.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.3%; Score 80; DB 6; Length 15;
Pred. No. 0.098;
RESULT 534
ID ABR33354 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1707.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.3%; Score 80; DB 6; Length 15;
Pred. No. 0.098;
RESULT 535
ID ABR33358 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1711.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.3%; Score 80; DB 6; Length 15;
Pred. No. 0.098;
RESULT 536
ID ABR3894 standard; protein; 156 AA.
DE Novel human diagnostic protein #18885.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HISE-) HISEQ INC.
Query Match
Best Local Similarity 7.2%; Score 79.5; DB 4; Length 156;
Pred. No. 3;
RESULT 537
ID ADN17692 standard; protein; 355 AA.
DE Bacterial polypeptide #345.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.2%; Score 79.5; DB 8; Length 355;
Pred. No. 9.3;
RESULT 538
ID ABG96381 standard; protein; 1890 AA.
DE Human ovarian cancer marker M612.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.2%; Score 79.5; DB 5; Length 1890;
Pred. No. 97;
RESULT 539
ID ADM12352 standard; protein; 1890 AA.
DE Human CA125 ovarian cancer antigen mucin 16 protein.
PN US200335594-A1.
PD 25-DEC-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79.5; DB 8; Length 1890;
Pred. No. 97;
RESULT 540
ID ADO38574 standard; protein; 1890 AA.
DE Ovarian cancer antigen CA125.
PN US2004058881-A1.
PD 25-MAR-2004.
PA (ANTI-) ANTIGEN EXPRESS INC.
Query Match
Best Local Similarity 7.2%; Score 79.5; DB 8; Length 1890;
Pred. No. 97;
RESULT 541
ID ADJ6747 standard; protein; 2234 AA.
DE Human MycG GST fusion protein amino acid sequence Seq1D20.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match
Best Local Similarity 7.2%; Score 79.5; DB 8; Length 2234;
Pred. No. 1.2e+02;
RESULT 542
ID ABR33288 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1641.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;
Pred. No. 0.13;
RESULT 543
ID ABR33298 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1651.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;
Pred. No. 0.13;
RESULT 544
ID ABR33412 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1765.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;
Pred. No. 0.13;
RESULT 545
ID ABR33103 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1321.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;
Pred. No. 0.13;
RESULT 546
ID ABR33319 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1672.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;
Pred. No. 0.13;
RESULT 547
ID ABR33305 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1658.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;
Pred. No. 0.13;
RESULT 548
ID ABR33355 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1708.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
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Query Match  
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
RESULT 549  
ID ABR33381 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1734.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
RESULT 550  
ID ABR33139 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1357.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 7.2%; Score 79; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
RESULT 551  
ID ABR32949 standard; protein; 1189 AA.  
DE Novel human diagnostic protein #12940.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.2%; Score 79; DB 4; Length 1189;  
Best Local Similarity 21.8%; Pred. No. 58;  
RESULT 552  
ID ABR71928 standard; protein; 2037 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42576.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 7.2%; Score 79; DB 4; Length 2037;  
Best Local Similarity 24.5%; Pred. No. 1.2e+02;  
RESULT 553  
ID ABR30978 standard; protein; 233 AA.  
DE Extracellular and transmembrane regions of 0772P.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 5; Length 233;  
Best Local Similarity 21.5%; Pred. No. 6.7;  
RESULT 554  
ID ADA08641 standard; protein; 233 AA.  
DE Human O772P partial protein #11.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 7; Length 233;  
Best Local Similarity 21.5%; Pred. No. 6.7;  
RESULT 555  
ID ADF08984 standard; peptide; 233 AA.  
DE Secreted ovarian carcinoma antigen seqid 488.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 7; Length 233;  
Best Local Similarity 21.5%; Pred. No. 6.7;  
RESULT 556  
ID ABR31025 standard; protein; 318 AA.  
DE Amino acid sequence of the 3' constant region of 0772P.  
PN WO200206317-A2.  
PD 24-JAN-2002.

PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 5; Length 318;  
Best Local Similarity 20.8%; Pred. No. 10;  
RESULT 557  
ID ADA08747 standard; protein; 318 AA.  
DE Human O772P constant region consensus sequence #1.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 7; Length 318;  
Best Local Similarity 20.8%; Pred. No. 10;  
RESULT 558  
ID ADF09090 standard; protein; 318 AA.  
DE Secreted ovarian carcinoma antigen seqid 594.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 7; Length 318;  
Best Local Similarity 20.8%; Pred. No. 10;  
RESULT 559  
ID AAB42399 standard; protein; 336 AA.  
DE Human ORFX ORF2163 polypeptide sequence SEQ ID NO:4326.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 3; Length 336;  
Best Local Similarity 22.1%; Pred. No. 11;  
RESULT 560  
ID AAB12555 standard; protein; 438 AA.  
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:390.  
PN WO200036107-A2.  
PD 22-JUN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 3; Length 438;  
Best Local Similarity 21.5%; Pred. No. 16;  
RESULT 561  
ID ABR30899 standard; protein; 438 AA.  
DE O772P clone 21008.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 5; Length 438;  
Best Local Similarity 21.5%; Pred. No. 16;  
RESULT 562  
ID ADA08543 standard; protein; 438 AA.  
DE Human ovarian carcinoma antigen O772P #3.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match  
Best Local Similarity 7.1%; Score 78.5; DB 7; Length 438;  
Best Local Similarity 21.5%; Pred. No. 16;  
RESULT 563  
ID ADF08886 standard; protein; 438 AA.

DE Secretd ovarian carcinoma antigen seqid 390.  
PN US2003124140-A1.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 7; Length 438;  
Best Local Similarity 21.5%; Pred. No. 16;  
RESULT 564  
ID ADG46173 standard; protein; 438 AA.  
DE Human ovarian carcinoma polypeptide #4.  
PN US2003165504-A1.  
PD 04-SEP-2003.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
Query Match 7.1%; Score 78.5; DB 7; Length 438;  
Best Local Similarity 21.5%; Pred. No. 16;  
RESULT 565  
ID AAB72289 standard; protein; 696 AA.  
DE Rat protein isolated from skin cells SEQ ID NO: 501.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 7.1%; Score 78.5; DB 5; Length 696;  
Best Local Similarity 19.7%; Pred. No. 31;  
RESULT 566  
ID AAB12554 standard; protein; 833 AA.  
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.  
PN WO200006107-A2.  
PD 22-JUN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 3; Length 833;  
Best Local Similarity 21.5%; Pred. No. 40;  
RESULT 567  
ID ABB30898 standard; protein; 833 AA.  
DE O772P clone 21003.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 5; Length 833;  
Best Local Similarity 21.5%; Pred. No. 40;  
RESULT 568  
ID ADA08542 standard; protein; 833 AA.  
DE Human ovarian carcinoma antigen O772P #2.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match 7.1%; Score 78.5; DB 7; Length 833;  
Best Local Similarity 21.5%; Pred. No. 40;  
RESULT 569  
ID ADF08885 standard; protein; 833 AA.  
DE Secretd ovarian carcinoma antigen seqid 389.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 7; Length 833;  
Best Local Similarity 21.5%; Pred. No. 40;  
RESULT 570  
ID ADG46172 standard; protein; 833 AA.  
DE Human ovarian carcinoma polypeptide #3.  
PN US2003165504-A1.  
PD 04-SEP-2003.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
Query Match 7.1%; Score 78.5; DB 7; Length 833;

Best Local Similarity 21.5%; Pred. No. 40;  
RESULT 571  
ID AAB12552 standard; protein; 914 AA.  
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.  
PN WO200006107-A2.  
PD 22-JUN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 3; Length 914;  
Best Local Similarity 21.5%; Pred. No. 45;  
RESULT 572  
ID AAB9203 standard; protein; 914 AA.  
DE Human ovarian tumour-derived antigen O772P.  
PN WO200140269-A2.  
PD 07-JUN-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 4; Length 914;  
Best Local Similarity 21.5%; Pred. No. 45;  
RESULT 573  
ID ABB30968 standard; protein; 914 AA.  
DE Hypothetical protein sequence for clone O772P.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 5; Length 914;  
Best Local Similarity 21.5%; Pred. No. 45;  
RESULT 574  
ID ABB30896 standard; protein; 914 AA.  
DE O772P protein.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 5; Length 914;  
Best Local Similarity 21.5%; Pred. No. 45;  
RESULT 575  
ID ADA08631 standard; protein; 914 AA.  
DE Human O772P partial protein #1.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match 7.1%; Score 78.5; DB 7; Length 914;  
Best Local Similarity 21.5%; Pred. No. 45;  
RESULT 576  
ID ADA08465 standard; protein; 914 AA.  
DE Human ovarian carcinoma antigen O772P.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match 7.1%; Score 78.5; DB 7; Length 914;  
Best Local Similarity 21.5%; Pred. No. 45;  
RESULT 577  
ID ADF08974 standard; protein; 914 AA.  
DE Secretd ovarian carcinoma antigen seqid 478.  
PN US2003124140-A1.

PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 7; Length 914;  
Best Local Similarity 21.5%; Pred. NO. 45;  
RESULT 578  
ID ADF08808 standard; protein; 914 AA.  
DE Secreted ovarian carcinoma antigen seqid 312.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 7; Length 914;  
Best Local Similarity 21.5%; Pred. NO. 45;  
RESULT 579  
ID ADG46095 standard; protein; 914 AA.  
DE Human ovarian carcinoma polypeptide #1.  
PN US2003165504-A1.  
PD 04-SEP-2003.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
Query Match 7.1%; Score 78.5; DB 7; Length 914;  
Best Local Similarity 21.5%; Pred. NO. 45;  
RESULT 580  
ID ADH40451 standard; protein; 914 AA.  
DE Human breast cancer associated polypeptide sequence #4.  
PN US2004101899-A1.  
PD 27-MAY-2004.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 8; Length 914;  
Best Local Similarity 21.5%; Pred. NO. 45;  
RESULT 581  
ID ABB58394 standard; protein; 970 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 1974.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.1%; Score 78.5; DB 4; Length 970;  
Best Local Similarity 24.5%; Pred. NO. 49;  
RESULT 582  
ID ABR31026 standard; protein; 3451 AA.  
DE Amino acid sequence containing consensus and 3' region of 0772P.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 5; Length 3451;  
Best Local Similarity 20.8%; Pred. NO. 2.9e+02;  
RESULT 583  
ID ADA08748 standard; protein; 3451 AA.  
DE Human O772P consensus sequence #1.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Query Match 7.1%; Score 78.5; DB 7; Length 3451;  
Best Local Similarity 20.8%; Pred. NO. 2.9e+02;  
RESULT 584  
ID ADF09091 standard; protein; 3451 AA.  
DE Secreted ovarian carcinoma antigen seqid 595.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.1%; Score 78.5; DB 7; Length 3451;  
Best Local Similarity 20.8%; Pred. NO. 2.9e+02;  
RESULT 585  
ID ABR33306 standard; peptide; 15 AA.

DE Human cancer-related protein 156P5C12 HLA peptide #1659.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 586  
ID ABR33421 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1774.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 587  
ID ABR33331 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1349.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 588  
ID ABR33312 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1665.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 589  
ID ABR33119 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1337.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 590  
ID ABR33368 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1721.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 591  
ID ABR33385 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1738.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 592  
ID ABR33453 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1806.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 593  
ID ABR33329 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1682.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.1%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.16;  
RESULT 594  
ID ABR3299 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1652.

PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 595  
ID ABR33342 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1695.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 596  
ID ABR33352 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1705.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 597  
ID ABR33364 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1717.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 598  
ID ABR33378 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1731.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 599  
ID ABR33410 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1763.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 600  
ID ABR33448 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1801.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 601  
ID ABR33090 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1308.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 602  
ID ABR33123 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1341.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 603  
ID ABR33140 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1358.  
PN WO200283921-A2.

PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 604  
ID ABR33145 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1363.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 605  
ID ABR33425 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1778.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 606  
ID ABR33117 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1335.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 607  
ID ABR33332 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1685.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 608  
ID ABR33362 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1715.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 609  
ID ABR33089 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1307.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 610  
ID ABR33418 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1771.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 611  
ID ABR33440 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1793.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.16;  
RESULT 612  
ID ABE8513 standard; protein; 300 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:196.  
PN WO200200717-A2.  
PD 03-JAN-2002.

PA (MAXY-) MAXYGEN INC.  
Query Match 7.1%; Score 78; DB 5; Length 300;  
Best Local Similarity 21.4%; Pred. No. 11;  
RESULT 613  
ID ADM18831 standard; protein; 300 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:196.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 7.1%; Score 78; DB 8; Length 300;  
Best Local Similarity 21.4%; Pred. No. 11;  
RESULT 614  
ID ABR08348 standard; protein; 343 AA.  
DE RTR-like G protein-coupled receptor, SEQ ID NO:3.  
PN WO200200699-A1.  
PD 03-JAN-2002.  
PA (FARB) BAYER AG.  
Query Match 7.1%; Score 78; DB 5; Length 343;  
Best Local Similarity 20.9%; Pred. No. 13;  
RESULT 615  
ID ABR73784 standard; protein; 343 AA.  
DE Rat RTR orphan receptor protein.  
PN US2002150980-A1.  
PD 17-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.1%; Score 78; DB 6; Length 343;  
Best Local Similarity 20.9%; Pred. No. 13;  
RESULT 616  
ID ADB12843 standard; protein; 343 AA.  
DE Rat orphan G protein-coupled receptor RTR.  
PN US2002192760-A1.  
PD 19-DEC-2002.  
PA (LIYY/) LI Y.  
PA (ROSE/) ROSEN C A.  
PA (GOCA/) GOCCAYNE J D.  
Query Match 7.1%; Score 78; DB 6; Length 343;  
Best Local Similarity 20.9%; Pred. No. 13;  
RESULT 617  
ID ABR39948 standard; protein; 354 AA.  
DE Human prostate selective polypeptide Pr498.  
PN WO2003014298-A2.  
PD 20-FEB-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 7.1%; Score 78; DB 6; Length 354;  
Best Local Similarity 21.0%; Pred. No. 14;  
RESULT 618  
ID AAB95230 standard; protein; 555 AA.  
DE Human protein sequence SEQ ID NO:17363.  
PN EPI074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.1%; Score 78; DB 4; Length 555;  
Best Local Similarity 21.0%; Pred. No. 26;  
RESULT 619  
ID AAE22147 standard; protein; 555 AA.  
DE Human TRNPR-9 protein.  
PN WO200226950-A2.  
PD 04-APR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.1%; Score 78; DB 5; Length 555;  
Best Local Similarity 21.0%; Pred. No. 26;  
RESULT 620  
ID ADG93389 standard; protein; 887 AA.  
DE Maize lipoxygenase (LOX) polypeptide #10.  
PN US200316685-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 7.1%; Score 78; DB 7; Length 887;  
Best Local Similarity 24.1%; Pred. No. 49;  
RESULT 621  
ID ADG93387 standard; protein; 887 AA.  
DE Maize lipoxygenase (LOX) polypeptide #9.  
PN US200316685-A1.

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PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 7.1%; Score 78; DB 7; Length 887;  
Best Local Similarity 24.1%; Pred. No. 49;  
RESULT 622  
ID AAM78602 standard; protein; 189 AA.  
DE Human protein SEQ ID NO 1264.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HXSE-) HXSEQ INC.  
Query Match 7.0%; Score 77.5; DB 4; Length 189;  
Best Local Similarity 19.5%; Pred. No. 6.5;  
RESULT 623  
ID ADP69604 standard; protein; 232 AA.  
DE Human REMAP protein - SEQ ID 33.  
PN WO2003048305-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.0%; Score 77.5; DB 7; Length 232;  
Best Local Similarity 23.3%; Pred. No. 8.6;  
RESULT 624  
ID AAY75166 standard; protein; 468 AA.  
DE Neisseria meningitidis ORF 585 protein sequence SEQ ID NO:1806.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 7.0%; Score 77.5; DB 3; Length 468;  
Best Local Similarity 23.2%; Pred. No. 23;  
RESULT 625  
ID ABR33096 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1314.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.0%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 626  
ID ABR33143 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1361.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.0%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 627  
ID ABR33380 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1733.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.0%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 628  
ID ABR33405 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1758.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.0%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 629  
ID ABR33286 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1639.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 7.0%; Score 77; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 630  
ID ABR33307 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1660.  
PN WO200283921-A2.



PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 631  
ID ABR33350 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1703.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 632  
ID ABR33359 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1712.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 633  
ID ABR33411 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1764.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 634  
ID ABR33353 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1706.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 635  
ID ABR33379 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1732.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 636  
ID ABR33111 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1329.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 637  
ID ABR33295 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1648.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 638  
ID ABR33403 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1756.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 639  
ID ABR33315 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1668.  
PN WO200283921-A2.  
PD 24-OCT-2002.

PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 640  
ID ABR33330 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1693.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 641  
ID ABR33442 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1795.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 642  
ID ABR33106 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1324.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 7.0%; Score 77; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.21;  
RESULT 643  
ID AAP0246 standard; protein; 282 AA.  
DE Sequence of mouse macrophage Fc-gamma-beta-2 receptor protein for  
DE immunoglobulin G (IgG).  
PN WO8803172-A.  
PD 05-MAY-1988.  
PA (SLOK) MEM SLOAN-KETTERING.  
PA (UYRO) UNIV ROCKEFELLER.  
Query Match  
Best Local Similarity 19.6%; Score 77; DB 1; Length 282;  
RESULT 644  
ID ABR6845 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NC5M) Protein SEQ ID NO:59.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC. 6.9%; Score 76.5; DB 5; Length 303;  
Query Match  
Best Local Similarity 22.6%; Pred. No. 16;  
RESULT 645  
ID ADM18694 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:59.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC. 6.9%; Score 76.5; DB 5; Length 303;  
Query Match  
Best Local Similarity 22.6%; Pred. No. 16;  
RESULT 646  
ID ABR73849 standard; protein; 314 AA.  
DE Candida albicans essential protein SEQ ID NO 7686.  
PN WO200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC. 6.9%; Score 76.5; DB 5; Length 314;  
Query Match  
Best Local Similarity 20.0%; Pred. No. 17;  
RESULT 647  
ID ADM6487 standard; protein; 436 AA.  
DE Thermococcus kodakarensis KOD1 protein sequence SeqID365.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP. 6.9%; Score 76.5; DB 8; Length 436;  
Query Match  
Best Local Similarity 22.6%; Pred. No. 27;  
RESULT 648  
ID AAE23281 standard; protein; 542 AA.  
DE Human deleted nectin-3alpha protein.  
PN WO200228902-A2.

PD 11-APR-2002.  
PA (IMMV-) IMMUNEX CORP. 6.9%; Score 76.5; DB 5; Length 542;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 36;  
RESULT 649  
ID AAE23283 standard; protein; 549 AA.  
DE Human nectin-3alpha protein.  
PN WO200228902-A2.  
PD 11-APR-2002.  
PA (IMMV-) IMMUNEX CORP. 6.9%; Score 76.5; DB 5; Length 549;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 37;  
RESULT 650  
ID AAE23282 standard; protein; 549 AA.  
DE Mouse nectin-3-human nectin 3alpha fusion protein.  
PN WO200228902-A2.  
PD 11-APR-2002.  
PA (IMMV-) IMMUNEX CORP. 6.9%; Score 76.5; DB 5; Length 549;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 37;  
RESULT 651  
ID ABR20222 standard; protein; 549 AA.  
DE Human IG gene related protein SEQ ID No 45.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC. 6.9%; Score 76.5; DB 6; Length 549;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 37;  
RESULT 652  
ID ADR66369 standard; protein; 549 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 223 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B. 6.9%; Score 76.5; DB 8; Length 549;  
PA (DAHL-) DAHL E. 6.9%; Score 76.5; DB 8; Length 549;  
PA (ROSE-) ROSENTHAL A. 6.9%; Score 76.5; DB 8; Length 549;  
PA (HERM-) HERMANN K. 6.9%; Score 76.5; DB 8; Length 549;  
PA (PILA-) PILARSKY C. 6.9%; Score 76.5; DB 8; Length 549;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 37;  
RESULT 653  
ID ADR66711 standard; protein; 549 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 223 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B. 6.9%; Score 76.5; DB 8; Length 549;  
PA (DAHL-) DAHL E. 6.9%; Score 76.5; DB 8; Length 549;  
PA (ROSE-) ROSENTHAL A. 6.9%; Score 76.5; DB 8; Length 549;  
PA (HERM-) HERMANN K. 6.9%; Score 76.5; DB 8; Length 549;  
PA (PILA-) PILARSKY C. 6.9%; Score 76.5; DB 8; Length 549;  
Query Match  
Best Local Similarity 25.4%; Pred. No. 37;  
RESULT 654  
ID ABR18352 standard; protein; 653 AA.  
DE Novel human diagnostic protein #18343.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. 6.9%; Score 76.5; DB 4; Length 653;  
Query Match  
Best Local Similarity 22.4%; Pred. No. 47;  
RESULT 655  
ID AD116948 standard; protein; 794 AA.  
DE African clawed frog NOVX protein homologue SegID 484.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CIRA-) CIRAAGEN CORP. 6.9%; Score 76.5; DB 5; Length 794;  
Query Match  
Best Local Similarity 19.2%; Pred. No. 62;  
RESULT 656  
ID ABR33335 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1688.  
PN WO200283921-A2.  
PD 24-OCT-2002.

PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 657  
ID ABR33377 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1730.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 658  
ID ABR33451 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1804.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 659  
ID ABR33318 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1671.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 660  
ID ABR33282 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1635.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 661  
ID ABR33437 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1790.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 662  
ID ABR33101 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1319.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 663  
ID ABR33086 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1304.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 664  
ID ABR33129 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1347.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.27;  
RESULT 665  
ID ABR33392 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1745.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. 6.9%; Score 76; DB 6; Length 15;

Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 666  
ID ABR33095 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1313.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 667  
ID ABR33415 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PC12 HLA peptide #1768.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 668  
ID ABR33114 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1332.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 669  
ID ABR33137 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1355.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 670  
ID ABR33336 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PC12 HLA peptide #1679.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 671  
ID ABR33102 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PID4 HLA peptide #1320.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 672  
ID ABR33316 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PC12 HLA peptide #1669.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 673  
ID ABR33439 standard; peptide; 15 AA.  
DE Human cancer-related protein 156PC12 HLA peptide #1792.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 76; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.27;  
RESULT 674  
ID ABR37802 standard; protein; 230 AA.  
DE Human mucin 1 transmembrane variant, MUC1/X protein.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 6.9%; Score 76; DB 6; Length 230;

Best Local Similarity 21.7%; Pred. NO. 12;  
RESULT 675  
ID ADI68550 standard; protein; 230 AA.  
DE Human heat mitochondrial protein as a therapeutic target SegID356.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 6.9%; Score 76; DB 7; Length 230;  
Best Local Similarity 21.7%; Pred. NO. 12;  
RESULT 676  
ID ADI57756 standard; protein; 230 AA.  
DE Human breast specific protein (BSF) #33.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 76; DB 8; Length 230;  
Best Local Similarity 21.7%; Pred. NO. 12;  
RESULT 677  
ID ADI57775 standard; protein; 232 AA.  
DE Human breast specific protein (BSF) #52.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 76; DB 8; Length 232;  
Best Local Similarity 23.1%; Pred. NO. 13;  
RESULT 678  
ID ABB89532 standard; protein; 127 AA.  
DE Human polyepitide SEQ ID NO 1908.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 127;  
Best Local Similarity 23.0%; Pred. NO. 6.2;  
RESULT 679  
ID AAM15391 standard; protein; 133 AA.  
DE Peptide #1825 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. NO. 6.6;  
RESULT 680  
ID ABB34397 standard; peptide; 133 AA.  
DE Peptide #1903 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. NO. 6.6;  
RESULT 681  
ID AAM7879 standard; protein; 133 AA.  
DE Peptide #1916 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. NO. 6.6;  
RESULT 682  
ID ABB29234 standard; peptide; 133 AA.  
DE Peptide #1885 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. NO. 6.6;  
RESULT 683  
ID ABB19808 standard; protein; 133 AA.  
DE Protein #1807 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;

Best Local Similarity 19.2%; Pred. No. 6.6;  
RESULT 684  
ID AAM67582 standard; protein: 133 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27888.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. No. 6.6;  
RESULT 685  
ID AAM55187 standard; protein: 133 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27922.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. No. 6.6;  
RESULT 686  
ID ABG49228 standard; peptide: 133 AA.  
DE Human liver peptide, SEQ ID No 27876.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. No. 6.6;  
RESULT 687  
ID AAM03153 standard; protein: 133 AA.  
DE Peptide #1835 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 4; Length 133;  
Best Local Similarity 19.2%; Pred. No. 6.6;  
RESULT 688  
ID ABG37173 standard; peptide: 133 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26838.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 133;  
Best Local Similarity 19.2%; Pred. No. 6.6;  
RESULT 689  
ID AD157774 standard; protein: 180 AA.  
DE Human breast specific protein (BSP) #51.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 180;  
Best Local Similarity 24.2%; Pred. No. 10;  
RESULT 690  
ID AAR89423 standard; protein: 239 AA.  
DE Mucin-derived protein MUC1/V/alt.  
PN WO9603502-A2.  
PD 08-FEB-1996.  
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 2; Length 239;  
Best Local Similarity 24.2%; Pred. No. 15;  
RESULT 691  
ID AAR89422 standard; protein: 240 AA.  
DE Mucin-derived protein MUC1/V.  
PN WO9603502-A2.  
PD 08-FEB-1996.  
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 2; Length 240;  
Best Local Similarity 24.2%; Pred. No. 15;  
RESULT 692  
ID ADE48140 standard; protein: 240 AA.  
DE MUC1/V protein.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 240;  
Best Local Similarity 24.2%; Pred. No. 15;

RESULT 693  
ID AD157768 standard; protein: 241 AA.  
DE Human breast specific protein (BSP) #45.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 241;  
Best Local Similarity 24.2%; Pred. No. 15;  
RESULT 694  
ID ADE48141 standard; protein: 249 AA.  
DE MUC1/V/alt protein.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 249;  
Best Local Similarity 24.2%; Pred. No. 16;  
RESULT 695  
ID AAR89420 standard; protein: 255 AA.  
DE Mucin-derived protein MUC1/Y.  
PN WO9603502-A2.  
PD 08-FEB-1996.  
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 2; Length 255;  
Best Local Similarity 24.2%; Pred. No. 16;  
RESULT 696  
ID ADA50573 standard; protein: 255 AA.  
DE Mucin 1 (MUC-1) splice variant #2 (MUC1Y), SEQ ID NO:28.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 255;  
Best Local Similarity 24.2%; Pred. No. 16;  
RESULT 697  
ID ADE48138 standard; protein: 255 AA.  
DE MUC1/Y protein.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 255;  
Best Local Similarity 24.2%; Pred. No. 16;  
RESULT 698  
ID AD157772 standard; protein: 255 AA.  
DE Human breast specific protein (BSP) #49.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 255;  
Best Local Similarity 24.2%; Pred. No. 16;  
RESULT 699  
ID AAR89421 standard; protein: 264 AA.  
DE Mucin-derived protein MUC1/Y/alt.  
PN WO9603502-A2.  
PD 08-FEB-1996.  
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 2; Length 264;  
Best Local Similarity 24.2%; Pred. No. 17;  
RESULT 700  
ID ADE48139 standard; protein: 264 AA.  
DE MUC1/Y/alt protein.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 264;  
Best Local Similarity 24.2%; Pred. No. 17;  
RESULT 701  
ID AD157767 standard; protein: 264 AA.  
DE Human breast specific protein (BSP) #44.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 264;  
Best Local Similarity 24.2%; Pred. No. 17;  
RESULT 702

ID AAR89418 standard; protein; 273 AA.  
DE Mucin-derived protein MUC1/X.  
PN WO9603502-A2.  
PD 08-FEB-1996.  
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 2; Length 273;  
Best Local Similarity 24.2%; Pred. No. 18;  
RESULT 703  
ID ADE48136 standard; protein; 273 AA.  
DE MUC1/X protein.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 273;  
Best Local Similarity 24.2%; Pred. No. 18;  
RESULT 704  
ID AD157753 standard; protein; 273 AA.  
DE Human breast specific protein (BSP) #30.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (D1AD-) D1ADDEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 273;  
Best Local Similarity 24.2%; Pred. No. 18;  
RESULT 705  
ID AAR89419 standard; protein; 282 AA.  
DE Mucin-derived protein MUC1/X/alt.  
PN WO9603502-A2.  
PD 08-FEB-1996.  
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 2; Length 282;  
Best Local Similarity 24.2%; Pred. No. 19;  
RESULT 706  
ID ADE48137 standard; protein; 282 AA.  
DE MUC1/X/alt protein.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 282;  
Best Local Similarity 24.2%; Pred. No. 19;  
RESULT 707  
ID ABP68563 standard; protein; 299 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:281.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 299;  
Best Local Similarity 21.6%; Pred. No. 20;  
RESULT 708  
ID ABP68445 standard; protein; 299 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:49.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 299;  
Best Local Similarity 21.6%; Pred. No. 20;  
RESULT 709  
ID ADM18684 standard; protein; 299 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:49.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 299;  
Best Local Similarity 21.6%; Pred. No. 20;  
RESULT 710  
ID ADM18916 standard; protein; 299 AA.  
DE Rabbit B7-1 protein SEQ ID NO:281.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 299;  
Best Local Similarity 21.6%; Pred. No. 20;  
RESULT 711  
ID ABP68509 standard; protein; 301 AA.

DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:192.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 301;  
Best Local Similarity 23.4%; Pred. No. 21;  
RESULT 712  
ID ADM18827 standard; protein; 301 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:192.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 301;  
Best Local Similarity 23.4%; Pred. No. 21;  
RESULT 713  
ID ABP68512 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:195.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 714  
ID ABP68536 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:219.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 715  
ID ABP68458 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:62.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 716  
ID ABP68530 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:213.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 717  
ID ABP68497 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:180.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 718  
ID ABP68520 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:203.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 719  
ID ADM18848 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:213.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 720  
ID ADM18854 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:219.

PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 721  
ID ADM18830 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:195.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 722  
ID ADM18697 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:62.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 723  
ID ADM18815 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:180.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 724  
ID ADM18838 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:203.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 725  
ID ABP68521 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SRO ID NO:204.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 303;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 726  
ID ABP68528 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:211.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 303;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 727  
ID ADM18839 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:204.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 303;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 728  
ID ADM18846 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:211.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 303;  
Best Local Similarity 21.6%; Pred. No. 21;  
RESULT 729  
ID AAU84810 standard; protein; 312 AA.  
DE Human MUC1R consensus sequence.  
PN WO200190197-A1.

PD 29-NOV-2001.  
PA (AUSU ) UNIV AUSTRALIAN NAT.  
Query Match 6.9%; Score 75.5; DB 5; Length 312;  
Best Local Similarity 24.2%; Pred. No. 22;  
RESULT 730  
ID AAB43416 standard; protein; 321 AA.  
DE Human cancer associated protein sequence SEQ ID NO:861.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.9%; Score 75.5; DB 3; Length 321;  
Best Local Similarity 24.2%; Pred. No. 23;  
RESULT 731  
ID AAR96298 standard; peptide; 327 AA.  
DE Glycoprotein 39 C terminal fragment.  
PN JP07051065-A.  
PD 28-FEB-1995.  
PA (NIKO-) NIPPON KOTAI KENKYUSHO KK.  
PA (UYKA-) UNIV KAGOSHIMA.  
Query Match 6.9%; Score 75.5; DB 2; Length 327;  
Best Local Similarity 24.2%; Pred. No. 23;  
RESULT 732  
ID ADP24569 standard; protein; 335 AA.  
DE PRO polypeptide SEQ ID NO:1747.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 335;  
Best Local Similarity 23.0%; Pred. No. 24;  
RESULT 733  
ID AAR27662 standard; protein; 348 AA.  
DE C-terminal region of H23-ETA-T antigen.  
PN WO9207000-A1.  
PD 30-APR-1992.  
PA (TRGE ) TRANSGENE SA.  
Query Match 6.9%; Score 75.5; DB 2; Length 348;  
Best Local Similarity 24.2%; Pred. No. 25;  
RESULT 734  
ID ADJ34832 standard; protein; 378 AA.  
DE Xylanase from an environmental sample seq id 48.  
PN WO2003106654-A2.  
PD 24-DEC-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 6.9%; Score 75.5; DB 8; Length 378;  
Best Local Similarity 20.1%; Pred. No. 28;  
RESULT 735  
ID ADG43994 standard; protein; 381 AA.  
DE Plasmid JMW389 gutted MUC-1 protein.  
PN WO200309193-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 381;  
Best Local Similarity 24.2%; Pred. No. 29;  
RESULT 736  
ID ADI57770 standard; protein; 420 AA.  
DE Human breast specific protein (BSP) #47.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 420;  
Best Local Similarity 24.2%; Pred. No. 33;  
RESULT 737  
ID ADI57752 standard; protein; 435 AA.  
DE Human breast specific protein (BSP) #29.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 435;  
Best Local Similarity 24.2%; Pred. No. 35;  
RESULT 738  
ID AAR23973 standard; protein; 455 AA.  
DE Transmembrane form of H23-ETA antigen.  
PN WO9207000-A1.

PD 30-APR-1992.  
PA (TRGE ) TRANSGENE SA.  
Query Match 6.9%; Score 75.5; DB 2; Length 455;  
Best Local Similarity 24.2%; Pred. No. 37;  
RESULT 739  
ID AAY71024 standard; protein; 455 AA.  
DE Human Mucin 1 (MUC-1) protein fragment #5.  
PN WO200025827-A2.  
PD 11-MAY-2000.  
PA (MENA ) MENARINI RICERCH SPA.  
Query Match 6.9%; Score 75.5; DB 3; Length 455;  
Best Local Similarity 24.2%; Pred. No. 37;  
RESULT 740  
ID ADE43996 standard; protein; 461 AA.  
DE Plasmid JMW399 MUC-1 protein.  
PN WO200309193-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 461;  
Best Local Similarity 24.2%; Pred. No. 38;  
RESULT 741  
ID ADI57750 standard; protein; 463 AA.  
DE Human breast specific protein (BSP) #27.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 463;  
Best Local Similarity 24.2%; Pred. No. 38;  
RESULT 742  
ID AAB09508 standard; protein; 473 AA.  
DE Human mucin-1 (MUC-1) protein.  
PN WO200157068-A1.  
PD 09-AUG-2001.  
PA (AUST-) AUSTIN RES INST.  
Query Match 6.9%; Score 75.5; DB 4; Length 473;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 743  
ID AAU00573 standard; protein; 475 AA.  
DE Human MUC1 polypeptide variant.  
PN WO200118035-A2.  
PD 15-MAR-2001.  
PA (TRGE ) TRANSGENE SA.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 6.9%; Score 75.5; DB 4; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 744  
ID ABB77476 standard; protein; 475 AA.  
DE Human MUC1 SEQ ID NO 3.  
PN WO200226765-A2.  
PD 04-APR-2002.  
PA (GERNA ) GENAISSANCE PHARM INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 745  
ID ADA50567 standard; protein; 475 AA.  
DE Mucin 1 (MUC-1), SEQ ID NO:22.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 746  
ID AAB37800 standard; protein; 475 AA.  
DE Human mucin 1 transmembrane variant, MUC1-VI protein.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 747  
ID ADD14120 standard; protein; 475 AA.  
DE Human src biomarker polypeptide SEQ ID NO:309.  
PD WO2003062395-A2.

PD 31-JUL-2003  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.9%; Score 75.5; DB 7; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 748  
ID ADB4813 standard; protein; 475 AA.  
DE MUC1 amino acid sequence.  
PN WO2003089451-A2.  
PD 30-OCT-2003.  
PA (DYAX-) DYAX CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 749  
ID ADB43992 standard; protein; 475 AA.  
DE Plasmid JMW283 MUC-1 protein.  
PN WO200309193-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 750  
ID ADF32626 standard; protein; 475 AA.  
DE Plasmid JMW283 MUC-1 amino acid sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 751  
ID ADI57746 standard; protein; 475 AA.  
DE Human breast specific protein (BSP) #23.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 752  
ID ADK70494 standard; protein; 475 AA.  
DE Respiratory disease differentially expressed protein #60.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 6.9%; Score 75.5; DB 8; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 753  
ID ADO28643 standard; protein; 475 AA.  
DE Human MUC1 protein SEQ ID NO:72.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GERTH ) GENENTECH INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 475;  
Best Local Similarity 24.2%; Pred. No. 39;  
RESULT 754  
ID ADF32628 standard; protein; 479 AA.  
DE Plasmid JMW358 MUC-1 amino acid sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 479;  
Best Local Similarity 24.2%; Pred. No. 40;  
RESULT 755  
ID ADI57761 standard; protein; 483 AA.  
DE Human breast specific protein (BSP) #38.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 483;  
Best Local Similarity 24.2%; Pred. No. 40;  
RESULT 756  
ID ADI57749 standard; protein; 484 AA.  
DE Human breast specific protein (BSP) #26.  
PN WO2003106648-A2.  
PD 24-DEC-2003.

PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 484;  
Best Local Similarity 24.2%; Pred. No. 40;  
RESULT 757  
ID AD157771 standard; protein; 485 AA.  
DE Human breast specific protein (BSP) #48.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 485;  
Best Local Similarity 24.2%; Pred. No. 40;  
RESULT 758  
ID AD157760 standard; protein; 492 AA.  
DE Human breast specific protein (BSP) #37.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 492;  
Best Local Similarity 24.2%; Pred. No. 41;  
RESULT 759  
ID AAU00539 standard; protein; 495 AA.  
DE Human MUC1 polypeptide.  
PN WO200118035-A2.  
PD 15-MAR-2001.  
PA (TRGE) TRANSGENE SA.  
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 6.9%; Score 75.5; DB 4; Length 495;  
Best Local Similarity 24.2%; Pred. No. 41;  
RESULT 760  
ID ADF32632 standard; protein; 495 AA.  
DE Plasmid JMW321 2x VNTR MUC-1 amino acid sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 495;  
Best Local Similarity 24.2%; Pred. No. 41;  
RESULT 761  
ID ABG96378 standard; protein; 515 AA.  
DE Human ovarian cancer marker OV45.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.9%; Score 75.5; DB 5; Length 515;  
Best Local Similarity 24.2%; Pred. No. 44;  
RESULT 762  
ID ADA50565 standard; protein; 515 AA.  
DE Human mucin 1 (MUC-1), SEQ ID NO:20.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 515;  
Best Local Similarity 24.2%; Pred. No. 44;  
RESULT 763  
ID ABR92123 standard; protein; 515 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:156.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 515;  
Best Local Similarity 24.2%; Pred. No. 44;  
RESULT 764  
ID AAG37797 standard; protein; 515 AA.  
DE Human mucin 1 transmembrane protein.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 515;  
Best Local Similarity 24.2%; Pred. No. 44;  
RESULT 765  
ID AD157743 standard; protein; 515 AA.  
DE Human breast specific protein (BSP) #20.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 517;  
Best Local Similarity 24.2%; Pred. No. 44;  
RESULT 766  
ID AD157742 standard; protein; 524 AA.  
DE Human breast specific protein (BSP) #19.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 524;  
Best Local Similarity 24.2%; Pred. No. 45;  
RESULT 769  
ID AD157751 standard; protein; 524 AA.  
DE Human breast specific protein (BSP) #28.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 524;  
Best Local Similarity 24.2%; Pred. No. 45;  
RESULT 770  
ID ABU14879 standard; protein; 549 AA.  
DE Protein encoded by Prokaryotic essential gene #406.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 549;  
Best Local Similarity 20.3%; Pred. No. 48;  
RESULT 771  
ID AAY71030 standard; protein; 577 AA.  
DE Ubiquitin-E. coli laci-human Mucin 1 fusion protein #5.  
PN WO200025827-A2.  
PD 11-MAY-2000.  
PA (MENA) MENARINI RICERCHE SPA.  
Query Match 6.9%; Score 75.5; DB 3; Length 577;  
Best Local Similarity 24.2%; Pred. No. 51;  
RESULT 772  
ID ADF32630 standard; protein; 595 AA.  
DE Plasmid JMW319 7x VNTR MUC-1 amino acid sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 595;  
Best Local Similarity 24.2%; Pred. No. 54;  
RESULT 773  
ID ADF32634 standard; protein; 599 AA.  
DE Plasmid JMW656 7x VNTR MUC-1 amino acid sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 599;  
Best Local Similarity 24.2%; Pred. No. 54;  
RESULT 774  
ID ADR89852 standard; protein; 599 AA.  
DE Human mucin MUC-1 with 7x VNTR.  
PN WO2004076655-A2.  
PD 10-SEP-2004.  
PA (GLAX) GLAXO GROUP LTD.



Query Match 6.9%; Score 75.5; DB 8; Length 599;  
Best Local Similarity 24.2%; Pred. No. 54;  
RESULT 775  
ID ADH10476 standard; protein; 656 AA.  
DE Human MUC-1-CPC fusion protein.  
PN WO2003104272-A1.  
PD 18-DEC-2003.  
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 656;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 776  
ID ADH10478 standard; protein; 678 AA.  
DE CPC-MUC-1 fusion protein.  
PN WO2003104272-A1.  
PD 18-DEC-2003.  
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 6.9%; Score 75.5; DB 8; Length 678;  
Best Local Similarity 24.2%; Pred. No. 64;  
RESULT 777  
ID ADC95237 standard; protein; 944 AA.  
DE E. faecium protein sequence SEQ ID 4864.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 944;  
Best Local Similarity 21.3%; Pred. No. 1e+02;  
RESULT 778  
ID ABP56040 standard; peptide; 1255 AA.  
DE MUC1 receptor (mucin 1 precursor) SEQ ID NO:10.  
PN WO200256022-A2.  
PD 18-JUL-2002.  
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.  
Query Match 6.9%; Score 75.5; DB 5; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 779  
ID ABB82568 standard; protein; 1255 AA.  
DE MUC1/REP transmembrane protein.  
PN WO200278598-A2.  
PD 10-OCT-2002.  
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.  
Query Match 6.9%; Score 75.5; DB 6; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 780  
ID ABR7537 standard; protein; 1255 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:311.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 781  
ID ABR92124 standard; protein; 1255 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:158.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.9%; Score 75.5; DB 6; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 782  
ID ADD45111 standard; protein; 1255 AA.  
DE Human Protein Q16615, SEQ ID NO 10544.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 6.9%; Score 75.5; DB 7; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 783  
ID ADE54622 standard; protein; 1255 AA.  
DE Human Protein Q16615, SEQ ID NO 427.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (FARB) BAYER AG.  
Query Match 6.9%; Score 75.5; DB 7; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 784  
ID ADQ29694 standard; protein; 1255 AA.  
DE Human colorectal cancer-associated protein #49.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 6.9%; Score 75.5; DB 8; Length 1255;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 785  
ID AD157740 standard; protein; 1256 AA.  
DE Human breast specific protein (BSP) #17.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.9%; Score 75.5; DB 8; Length 1256;  
Best Local Similarity 24.2%; Pred. No. 1.5e+02;  
RESULT 786  
ID ABB65886 standard; protein; 1279 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24450.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.9%; Score 75.5; DB 4; Length 1279;  
Best Local Similarity 24.0%; Pred. No. 1.6e+02;  
RESULT 787  
ID ABB7362 standard; protein; 1713 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37878.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.9%; Score 75.5; DB 4; Length 1713;  
Best Local Similarity 24.1%; Pred. No. 2.4e+02;  
RESULT 788  
ID AANJ8981 standard; protein; 1713 AA.  
DE Drosophila G-protein coupled receptor, GCPR #59.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.9%; Score 75.5; DB 4; Length 1713;  
Best Local Similarity 24.1%; Pred. No. 2.4e+02;  
RESULT 789  
ID ADC35925 standard; protein; 1713 AA.  
DE Drosophila G protein coupled receptor seq id 61.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLEPERA CORP.  
Query Match 6.9%; Score 75.5; DB 7; Length 1713;  
Best Local Similarity 24.1%; Pred. No. 2.4e+02;  
RESULT 790  
ID ABR33128 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1346.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 791  
ID ABR33360 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1713.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 792  
ID ABR33127 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1345.

PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 793  
ID ABR33334 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1687.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 794  
ID ABR33340 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1693.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 795  
ID ABR33342 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1360.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 796  
ID ABR33144 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1362.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 797  
ID ABR33357 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1710.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 798  
ID ABR33292 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1645.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 799  
ID ABR33339 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1692.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 800  
ID ABR33441 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1794.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.8%; Score 75; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
RESULT 801  
ID ADO29551 standard; protein: 343 AA.  
DE Mouse GPCR MRCF, SEQ ID NO:653.  
PN WO200404000-A2.

PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.8%; Score 75; DB 8; Length 343;  
Best Local Similarity 20.9%; Pred. No. 28;  
RESULT 802  
ID ADS08193 standard; protein: 548 AA.  
DE Staphylococcus epidermis polypeptide seqid 7488.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Query Match 6.8%; Score 75; DB 8; Length 548;  
Best Local Similarity 32.7%; Pred. No. 54;  
RESULT 803  
ID ABG06933 standard; protein: 562 AA.  
DE Novel human diagnostic protein #6924.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.8%; Score 75; DB 4; Length 562;  
Best Local Similarity 22.1%; Pred. No. 56;  
RESULT 804  
ID AAY81803 standard; protein: 1260 AA.  
DE Wild type (C57BL/6J) murine mahogany protein sequence.  
PN WO200005373-A2.  
PD 03-FEB-2000.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.8%; Score 75; DB 3; Length 1260;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 805  
ID ADE58694 standard; protein: 1472 AA.  
DE Rat Protein NP\_033860, SEQ ID NO 4570.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GHEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 6.8%; Score 75; DB 7; Length 1472;  
Best Local Similarity 19.6%; Pred. No. 2.2e+02;  
RESULT 806  
ID ABP5658 standard; protein: 204 AA.  
DE Chimpanzee C68 adenovirus E3 22.3 kDa protein SEQ ID NO:23.  
PN WO2003000851-A2.  
PD 03-JAN-2003.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 6.8%; Score 74.5; DB 6; Length 204;  
Best Local Similarity 18.1%; Pred. No. 15;  
RESULT 807  
ID AAU11389 standard; protein: 307 AA.  
DE Human T2R71 (hT2R71) polypeptide.  
PN WO200177676-A1.  
PD 18-OCT-2001.  
PA (SENO-) SENOMYX INC.  
Query Match 6.8%; Score 74.5; DB 5; Length 307;  
Best Local Similarity 23.7%; Pred. No. 27;  
RESULT 808  
ID ABP95935 standard; protein: 307 AA.  
DE Human GPCR polypeptide SEQ ID NO 680.  
PN WO200216548-A2.  
PD 28-FEB-2002.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 6.8%; Score 74.5; DB 5; Length 307;  
Best Local Similarity 23.7%; Pred. No. 27;  
RESULT 809  
ID ADC6899 standard; protein: 307 AA.  
DE Human GPCR protein SEQ ID NO:1442.  
PN EPI270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 6.8%; Score 74.5; DB 7; Length 307;  
Best Local Similarity 23.7%; Pred. No. 27;  
RESULT 810  
ID ADR29250 standard; protein: 307 AA.

DE Taste receptor modulation-related human T2R71 protein sequence SeqID189.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENO-) SENOMYX INC.  
Query Match  
Best Local Similarity 6.8%; Score 74.5; DB 8; Length 307;  
PRED. NO. 27;  
RESULT 811  
ID ADM33293 standard; protein; 307 AA.  
DE Human bitter taste receptor TAS2R41 protein SEQ ID NO:7.  
PN WO2004029087-A2.  
PD 08-APR-2004.  
PA (DEBR-) DEUT INST ERNAERUNGSPORSCHUNG POTSDAM.  
Query Match  
Best Local Similarity 6.8%; Score 74.5; DB 8; Length 307;  
PRED. NO. 27;  
RESULT 812  
ID ABR92523 standard; protein; 664 AA.  
DE Heridically active polypeptide SEQ ID NO 1734.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 6.8%; Score 74.5; DB 5; Length 664;  
PRED. NO. 81;  
RESULT 813  
ID ABR33135 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1353.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 814  
ID ABR33303 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1656.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 815  
ID ABR33361 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1714.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 816  
ID ABR33394 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1747.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 817  
ID ABR33374 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1727.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 818  
ID ABR33338 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1691.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 819  
ID ABR33401 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1754.

PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 820  
ID ABR33091 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1309.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 821  
ID ABR33134 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1352.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 822  
ID ABR33417 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1770.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 823  
ID ABR33356 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1709.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 824  
ID ABR33110 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1328.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 825  
ID ABR33396 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1749.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 826  
ID ABR333426 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1779.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 827  
ID ABR33320 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1673.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 6.7%; Score 74; DB 6; Length 15;  
PRED. NO. 0.46;  
RESULT 828  
ID ABR33308 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1661.  
PN WO200283921-A2.

PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.7%; Score 74; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.46;  
RESULT 829  
ID ABR33393 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1646.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.7%; Score 74; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.46;  
RESULT 830  
ID ABR33333 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1686.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.7%; Score 74; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.46;  
RESULT 831  
ID ABR27051 standard; protein; 494 AA.  
DE Streptococcus polypeptide SEQ ID NO 3278.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.7%; Score 74; DB 5; Length 494;  
Best Local Similarity 23.3%; Pred. No. 61;  
RESULT 832  
ID ADS4484 standard; protein; 589 AA.  
DE Bacterial polypeptide #23314.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.7%; Score 74; DB 8; Length 589;  
Best Local Similarity 24.0%; Pred. No. 78;  
RESULT 833  
ID AD15757 standard; protein; 614 AA.  
DE Human breast specific protein (BSP) #34.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 6.7%; Score 74; DB 8; Length 614;  
Best Local Similarity 22.5%; Pred. No. 82;  
RESULT 834  
ID AD18689 standard; protein; 1005 AA.  
DE Human cell adhesion and extracellular matrix CADECM-16 protein - SEQ 16.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 6.7%; Score 74; DB 8; Length 1005;  
Best Local Similarity 28.6%; Pred. No. 1.6e+02;  
RESULT 835  
ID ABR58398 standard; protein; 154 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 1986.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.7%; Score 73.5; DB 4; Length 154;  
Best Local Similarity 34.8%; Pred. No. 14;  
RESULT 836  
ID AAR48755 standard; protein; 298 AA.  
DE Human thoracic aorta G-protein coupled receptor protein.  
PN WO9405695-A1.  
PD 17-MAR-1994.  
PA (UNYV ) UNIV NEW YORK STATE.  
Query Match 6.7%; Score 73.5; DB 2; Length 298;  
Best Local Similarity 21.0%; Pred. No. 34;

RESULT 837  
ID AAW02727 standard; peptide; 298 AA.  
DE Human thoracic aorta G-protein coupled receptor.  
PN US5508384-A.  
PD 16-APR-1996.  
PA (UNYV ) UNIV NEW YORK STATE.  
Query Match 6.7%; Score 73.5; DB 2; Length 298;  
Best Local Similarity 21.0%; Pred. No. 34;  
RESULT 838  
ID ABR68446 standard; protein; 299 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:50.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 5; Length 299;  
Best Local Similarity 21.6%; Pred. No. 34;  
RESULT 839  
ID ADM18685 standard; protein; 299 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:50.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 8; Length 299;  
Best Local Similarity 21.6%; Pred. No. 34;  
RESULT 840  
ID ABR68505 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:188.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 5; Length 303;  
Best Local Similarity 21.6%; Pred. No. 35;  
RESULT 841  
ID ABR68517 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:200.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 5; Length 303;  
Best Local Similarity 21.6%; Pred. No. 35;  
RESULT 842  
ID ABR68518 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:201.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 5; Length 303;  
Best Local Similarity 21.6%; Pred. No. 35;  
RESULT 843  
ID ADM18835 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:200.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 8; Length 303;  
Best Local Similarity 21.6%; Pred. No. 35;  
RESULT 844  
ID ADM18836 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:201.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 8; Length 303;  
Best Local Similarity 21.6%; Pred. No. 35;  
RESULT 845  
ID ADM18823 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:188.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.7%; Score 73.5; DB 8; Length 303;  
Best Local Similarity 21.6%; Pred. No. 35;  
RESULT 846

ID ABB48941 standard; protein; 321 AA.  
DE Listeria monocytogenes protein #1645.  
PN W0200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match 6.7%; Score 73.5; DB 5; Length 321;  
Best Local Similarity 21.8%; Pred. No. 38;  
RESULT 847  
ID ABR53819 standard; protein; 465 AA.  
DE Protein sequence #SEQ ID 2503.  
PN EPI258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 6.7%; Score 73.5; DB 6; Length 465;  
Best Local Similarity 20.0%; Pred. No. 63;  
RESULT 848  
ID ADK65004 standard; protein; 465 AA.  
DE Disease treating protein complex-derived protein #1514.  
PN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 6.7%; Score 73.5; DB 7; Length 465;  
Best Local Similarity 20.0%; Pred. No. 63;  
RESULT 849  
ID ADN24173 standard; protein; 488 AA.  
DE Bacterial polypeptide #6826.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.7%; Score 73.5; DB 8; Length 488;  
Best Local Similarity 21.3%; Pred. No. 68;  
RESULT 850  
ID ADN26366 standard; protein; 498 AA.  
DE Bacterial polypeptide #9019.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.7%; Score 73.5; DB 8; Length 498;  
Best Local Similarity 19.2%; Pred. No. 70;  
RESULT 851  
ID ABU32150 standard; protein; 547 AA.  
DE Protein encoded by Prokaryotic essential gene #17677.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.7%; Score 73.5; DB 6; Length 547;  
Best Local Similarity 19.8%; Pred. No. 80;  
RESULT 852  
ID ABO62057 standard; protein; 562 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8574.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.7%; Score 73.5; DB 7; Length 562;  
Best Local Similarity 19.8%; Pred. No. 83;  
RESULT 853  
ID AD025508 standard; protein; 630 AA.  
DE Binding domain-immunoglobulin fusion protein-associated protein #31.  
PN US2003118592-A1.  
PD 26-JUN-2003.  
PA (GENE-) GENECAFT INC.  
Query Match 6.7%; Score 73.5; DB 7; Length 630;  
Best Local Similarity 19.1%; Pred. No. 97;  
RESULT 854  
ID ADM26406 standard; protein; 656 AA.

DE Hyperthermophile Mechanopyrus kandleri protein #1012.  
PN W02003076575-A2.  
PD 18-SEP-2003.  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY/) MALYKH A.  
Query Match 6.7%; Score 73.5; DB 7; Length 656;  
Best Local Similarity 23.8%; Pred. No. 1e+02;  
RESULT 855  
ID ABB97543 standard; protein; 785 AA.  
DE Novel human Protein SEQ ID NO: 811.  
PN W0200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.7%; Score 73.5; DB 5; Length 785;  
Best Local Similarity 18.6%; Pred. No. 1.3e+02;  
RESULT 856  
ID AAR49730 standard; protein; 796 AA.  
DE Sequence encoded by murine OSF-4 CDNA.  
PN EP585801-A2.  
PD 09-MAR-1994.  
PA (FARH) HOECHST JAPAN LTD.  
Query Match 6.7%; Score 73.5; DB 2; Length 796;  
Best Local Similarity 21.7%; Pred. No. 1.3e+02;  
RESULT 857  
ID AAB60418 standard; protein; 796 AA.  
DE Mouse PrP-binding protein, OB-cadherin-1.  
PN W0200100235-A1.  
PD 04-JAN-2001.  
PA (UYMC-) UNIV MCGILL.  
PA (CAPR-) CAPRION PHARM INC.  
Query Match 6.7%; Score 73.5; DB 4; Length 796;  
Best Local Similarity 21.7%; Pred. No. 1.3e+02;  
RESULT 858  
ID ABB57294 standard; protein; 796 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO: 826.  
PN W0200188188-A2.  
PD 22-NOV-2001.  
PA (UNVI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 6.7%; Score 73.5; DB 5; Length 796;  
Best Local Similarity 21.7%; Pred. No. 1.3e+02;  
RESULT 859  
ID AD116949 standard; protein; 796 AA.  
DE Murine NOVX protein homologue SeqID 485.  
PN W0200268649-A2.  
PD 06-SEP-2002.  
PA (CUNA-) CUPAGEN CORP.  
Query Match 6.7%; Score 73.5; DB 5; Length 796;  
Best Local Similarity 21.7%; Pred. No. 1.3e+02;  
RESULT 860  
ID AAB18268 standard; protein; 1166 AA.  
DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:125.  
PN W0200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 6.7%; Score 73.5; DB 3; Length 1166;  
Best Local Similarity 22.1%; Pred. No. 2.3e+02;  
RESULT 861  
ID AAY04157 standard; peptide; 14 AA.  
DE Human secreted protein 5' EST signal peptide SEQ ID NO:28.  
PN W09906439-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 862  
ID AAY11373 standard; protein; 14 AA.  
DE Human 5' EST secreted protein SEQ ID NO:28.  
PN W09906551-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.

Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 863  
ID AAY04175 standard; peptide: 14 AA.  
DE Human secreted protein 5' EST signal peptide SEQ ID NO:28.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 864  
ID AAY12520 standard; peptide: 14 AA.  
DE Human 5' EST signal peptide SEQ ID NO: 28 from WO 9906553.  
PN WO9906553-A2.  
PD 11-FEB-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 865  
ID AAY35891 standard; peptide: 14 AA.  
DE Signal peptide of extended secreted protein, SEQ ID NO. 28.  
PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 866  
ID AAY59652 standard; peptide: 14 AA.  
DE Secreted protein extended EST signal peptide #6.  
PN WO9940189-A2.  
PD 12-AUG-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 867  
ID AAY25460 standard; peptide: 14 AA.  
DE Human secreted protein 6 signal peptide derived from extended cDNA.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 868  
ID AAY12679 standard; peptide: 14 AA.  
DE Human 5' EST secreted protein signal peptide.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 869  
ID AAY11715 standard; protein: 14 AA.  
DE Peptide encoded by extended cDNA derived from 5' EST.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 870  
ID AAY64646 standard; peptide: 14 AA.  
DE Human 58-35-2-F10-F12 signal peptide.  
PN WO9953051-A2.  
PD 21-OCT-1999.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 871  
ID AAG00015 standard; peptide: 14 AA.  
DE Human secreted protein #3 signal peptide.  
PN EPI033401-A2.  
PD 06-SEP-2000.  
PA (G8ST ) GENSET.  
Query Match 6.6%; Score 73; DB 3; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 872  
ID ADJ45875 standard; peptide: 14 AA.  
DE Novel human secreted protein-related peptide sequence SeqID28.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUC/) DUCLEERT A.  
PA (BOUG/) BOUGLEERT L.  
Query Match 6.6%; Score 73; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 873  
ID ADM77747 standard; peptide: 14 AA.  
DE Signal sequence #6.  
PN US2003162176-A1.  
PD 28-AUG-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUC/) DUCLEERT A.  
PA (BOUG/) BOUGLEERT L.  
Query Match 6.6%; Score 73; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
RESULT 874  
ID ABR33399 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1752.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 875  
ID ABR33407 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1760.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 876  
ID ABR33446 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1799.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 877  
ID ABR33366 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1719.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 878  
ID ABR33409 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1762.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 879  
ID ABR33085 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1303.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 880  
ID ABR33094 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1312.  
PN WO200283921-A2.

PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 881  
ID ABR33349 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1702.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.6%; Score 73; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
RESULT 882  
ID ADP07700 standard; protein; 195 AA.  
DE Bacterial polypeptide #3813.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.6%; Score 73; DB 7; Length 195;  
Best Local Similarity 21.8%; Pred. No. 21;  
RESULT 883  
ID AAR85151 standard; protein; 205 AA.  
DE Endothelial cell polypeptide.  
PN EP682113-A2.  
PD 15-NOV-1995.  
PA (ONOX) ONO PHARM CO LTD.  
Query Match 6.6%; Score 73; DB 2; Length 205;  
Best Local Similarity 19.1%; Pred. No. 23;  
RESULT 884  
ID AAM78603 standard; protein; 205 AA.  
DE Human protein SEQ ID NO 1265.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.6%; Score 73; DB 4; Length 205;  
Best Local Similarity 19.1%; Pred. No. 23;  
RESULT 885  
ID ABR43432 standard; protein; 205 AA.  
DE Human malignant neoplasm related protein SEQ ID NO:14.  
PN WO2003025135-A2.  
PD 27-MAR-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 6.6%; Score 73; DB 6; Length 205;  
Best Local Similarity 19.1%; Pred. No. 23;  
RESULT 886  
ID ADF61798 standard; protein; 205 AA.  
DE Human D1-1 protein.  
PN WO2003091447-A2.  
PD 06-NOV-2003.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 6.6%; Score 73; DB 7; Length 205;  
Best Local Similarity 19.1%; Pred. No. 23;  
RESULT 887  
ID ADE77093 standard; protein; 205 AA.  
DE Human protein expressed in a liver disorder #68.  
PN US2003108871-A1.  
PD 12-JUN-2003.  
PA (KASE) KASER M R.  
Query Match 6.6%; Score 73; DB 8; Length 205;  
Best Local Similarity 19.1%; Pred. No. 23;  
RESULT 888  
ID AAB38332 standard; protein; 206 AA.  
DE Human secreted protein encoded by gene 2 clone HEMRQ46.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.6%; Score 73; DB 3; Length 206;  
Best Local Similarity 19.1%; Pred. No. 23;  
RESULT 889  
ID AAB88895 standard; protein; 221 AA.  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 603.  
PN WO200055173-A1.  
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.6%; Score 73; DB 3; Length 221;  
Best Local Similarity 19.1%; Pred. No. 25;  
RESULT 890  
ID AAM79587 standard; protein; 238 AA.  
DE Human protein SEQ ID NO 3233.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.6%; Score 73; DB 4; Length 238;  
Best Local Similarity 19.1%; Pred. No. 28;  
RESULT 891  
ID AAM79586 standard; protein; 238 AA.  
DE Human protein SEQ ID NO 3232.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.6%; Score 73; DB 4; Length 238;  
Best Local Similarity 19.1%; Pred. No. 28;  
RESULT 892  
ID ADN47010 standard; protein; 254 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID888.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 6.6%; Score 73; DB 8; Length 254;  
Best Local Similarity 32.4%; Pred. No. 31;  
RESULT 893  
ID ADR99905 standard; protein; 272 AA.  
DE Immune Response Associated Protein, IRAP-13, SEQ ID 13.  
PN WO2004081197-A2.  
PD 23-SEP-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.6%; Score 73; DB 8; Length 272;  
Best Local Similarity 20.9%; Pred. No. 34;  
RESULT 894  
ID AAU75544 standard; protein; 370 AA.  
DE Mouse B7-1like protein, B7-L\_m1.  
PN WO200200710-A2.  
PD 03-JAN-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 6.6%; Score 73; DB 5; Length 370;  
Best Local Similarity 22.4%; Pred. No. 52;  
RESULT 895  
ID ABU35478 standard; protein; 512 AA.  
DE Protein encoded by Prokaryotic essential gene #21005.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.6%; Score 73; DB 6; Length 512;  
Best Local Similarity 21.8%; Pred. No. 82;  
RESULT 896  
ID ABG29239 standard; protein; 979 AA.  
DE Novel human diagnostic protein #29230.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.6%; Score 73; DB 4; Length 979;  
Best Local Similarity 23.7%; Pred. No. 2e+02;  
RESULT 897  
ID ADD49069 standard; protein; 1147 AA.  
DE Human NOV1a SEQ ID 42.  
PN WO2003060149-A2.  
PD 24-JUL-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.6%; Score 73; DB 7; Length 1147;  
Best Local Similarity 23.7%; Pred. No. 2.5e+02;  
RESULT 898  
ID ADH71108 standard; protein; 1147 AA.  
DE Human protein of the invention NOV2a SEQ ID NO:4.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.

Query Match 6.6%; Score 73; DB 8; Length 1147;  
Best Local Similarity 23.7%; Pred. No. 2.5e+02;  
RESULT 899  
ID ABO84632 standard; protein: 1147 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4195.  
PN WO2004074320-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.6%; Score 73; DB 8; Length 1147;  
Best Local Similarity 23.7%; Pred. No. 2.5e+02;  
RESULT 900  
ID ABO84632 standard; protein: 1179 AA.  
DE Human cancer-associated protein HP18-037.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 6.6%; Score 73; DB 8; Length 1179;  
Best Local Similarity 23.7%; Pred. No. 2.6e+02;  
RESULT 901  
ID ABO03548 standard; protein: 1181 AA.  
DE Angiogenesis-associated human protein sequence #93.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.6%; Score 73; DB 6; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 902  
ID ABR59703 standard; protein: 1181 AA.  
DE Human VLA-2 receptor alpha 2 subunit.  
PN WO2003029277-A2.  
PD 10-APR-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.6%; Score 73; DB 6; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 903  
ID AAG79775 standard; protein: 1181 AA.  
DE Alpha2 integrin.  
PN WO2002101070-A2.  
PD 19-DEC-2002.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.6%; Score 73; DB 6; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 904  
ID ABO03616 standard; protein: 1181 AA.  
DE Human expressed protein tag (EPT) #282.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.6%; Score 73; DB 6; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 905  
ID ABO03614 standard; protein: 1181 AA.  
DE Human expressed protein tag (EPT) #280.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.6%; Score 73; DB 6; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 906  
ID ABO03617 standard; protein: 1181 AA.  
DE Human expressed protein tag (EPT) #283.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.6%; Score 73; DB 6; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 907  
ID ADU39968 standard; protein: 1181 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C338.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.6%; Score 73; DB 7; Length 1181;

Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 908  
ID ABO84633 standard; protein: 1181 AA.  
DE Human cancer-associated protein HP18-037.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 6.6%; Score 73; DB 8; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 909  
ID ADR46664 standard; protein: 1181 AA.  
DE Cancer-associated protein, SEQ ID 77.  
PN WO2004073657-A2.  
PD 02-SEP-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.6%; Score 73; DB 8; Length 1181;  
Best Local Similarity 23.7%; Pred. No. 2.7e+02;  
RESULT 910  
ID ADN22950 standard; protein: 231 AA.  
DE Bacterial polypeptide #5603.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.6%; Score 72.5; DB 8; Length 231;  
Best Local Similarity 22.4%; Pred. No. 31;  
RESULT 911  
ID ADA50577 standard; protein: 252 AA.  
DE Mucin 1 (MUC-1) splice variant #4 (MUC1Y variant), SEQ ID NO:32.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 6.6%; Score 72.5; DB 6; Length 252;  
Best Local Similarity 23.1%; Pred. No. 35;  
RESULT 912  
ID AAE37798 standard; protein: 252 AA.  
DE Human mucin 1 transmembrane variant, MUC1/Y protein.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 6.6%; Score 72.5; DB 6; Length 252;  
Best Local Similarity 23.1%; Pred. No. 35;  
RESULT 913  
ID ABB68579 standard; protein: 302 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:272.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.6%; Score 72.5; DB 5; Length 302;  
Best Local Similarity 21.6%; Pred. No. 45;  
RESULT 914  
ID ADM18907 standard; protein: 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:272.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.6%; Score 72.5; DB 8; Length 302;  
Best Local Similarity 21.6%; Pred. No. 45;  
RESULT 915  
ID ABB68457 standard; protein: 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:61.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.6%; Score 72.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 45;  
RESULT 916  
ID ABB68502 standard; protein: 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:185.  
PN WO200200717-A2.



PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC. 6.6%; Score 72.5; DB 5; Length 303;  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45;  
RESULT 917  
ID ABP68585 standard; protein: 303 AA.  
DE Human co-stimulatory molecule (NCSCM) Protein SEQ ID NO:283.  
PN WO2000200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 918  
ID ABP68510 standard; protein: 303 AA.  
DE Novel co-stimulatory molecule (NCSCM) Protein SEQ ID NO:193.  
PN WO2000200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 919  
ID ABP68503 standard; protein: 303 AA.  
DE Novel co-stimulatory molecule (NCSCM) Protein SEQ ID NO:186.  
PN WO2000200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 920  
ID ABP68514 standard; protein: 303 AA.  
DE Novel co-stimulatory molecule (NCSCM) Protein SEQ ID NO:197.  
PN WO2000200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 921  
ID ADM18918 standard; protein: 303 AA.  
DE Co-stimulatory molecule consensus CD28BP protein SEQ ID NO:283.  
PN WO20004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 922  
ID ADM18821 standard; protein: 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:186.  
PN WO20004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 923  
ID ADM18820 standard; protein: 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:185.  
PN WO20004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 924  
ID ADM18828 standard; protein: 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:193.  
PN WO20004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 925  
ID ADM18832 standard; protein: 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:197.  
PN WO20004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 926  
ID ADM18696 standard; protein: 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:61.  
PN WO20004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match  
Best Local Similarity 24.6%; Pred. No. 45; Length 303;  
RESULT 927  
ID ABP92521 standard; protein: 682 AA.  
DE Hericidially active polypeptide SEQ ID NO 1732.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 23.7%; Pred. No. 1.4e+02; Length 682;  
RESULT 928  
ID ABM69149 standard; protein: 912 AA.  
DE Photornabidus luminescens protein sequence #2246.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 22.1%; Pred. No. 2.1e+02; Length 912;  
RESULT 929  
ID ABR33121 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1339.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.76; Length 15;  
RESULT 930  
ID ABR33133 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1351.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.76; Length 15;  
RESULT 931  
ID ABR33376 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1729.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.76; Length 15;  
RESULT 932  
ID ABR33423 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1776.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.76; Length 15;  
RESULT 933  
ID ABR33088 standard; peptide: 15 AA.  
DE Human cancer-related protein 156P1D4 HLA peptide #1306.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.76; Length 15;  
RESULT 934  
ID AAB74745 standard; protein: 157 AA.  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:54.  
PN WO200112775-A2.  
PD 22-FEB-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 72; DB 4; Length 157;  
Best Local Similarity 22.3%; Pred. No. 20;  
RESULT 935  
ID ABG65312 standard; protein; 157 AA.  
DE Human albumin fusion protein #1987.  
PN WO20017137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 72; DB 5; Length 157;  
Best Local Similarity 22.3%; Pred. No. 20;  
RESULT 936  
ID ADL78579 standard; protein; 157 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 2061.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 6.5%; Score 72; DB 8; Length 157;  
Best Local Similarity 22.3%; Pred. No. 20;  
RESULT 937  
ID AAB74768 standard; protein; 185 AA.  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:77.  
PN WO200112775-A2.  
PD 22-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 72; DB 4; Length 185;  
Best Local Similarity 22.3%; Pred. No. 26;  
RESULT 938  
ID ADS85091 standard; protein; 293 AA.  
DE Mouse atopic dermatitis-related protein sequence SeqID93.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUJUTENDO.  
Query Match 6.5%; Score 72; DB 8; Length 293;  
Best Local Similarity 20.0%; Pred. No. 49;  
RESULT 939  
ID ADL04462 standard; protein; 510 AA.  
DE M. catarrhalis protein #228.  
PN US679310-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.5%; Score 72; DB 8; Length 510;  
Best Local Similarity 19.6%; Pred. No. 1.1e+02;  
RESULT 940  
ID ABB71280 standard; protein; 588 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40632.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.5%; Score 72; DB 4; Length 588;  
Best Local Similarity 25.8%; Pred. No. 1.3e+02;  
RESULT 941  
ID AAY28606 standard; protein; 653 AA.  
DE cc359\_4 secreted protein.  
PN WO9950405-A1.  
PD 07-OCT-1999.  
PA (GEMY) GENETICS INST INC.  
Query Match 6.5%; Score 72; DB 2; Length 653;  
Best Local Similarity 20.3%; Pred. No. 1.5e+02;  
RESULT 942  
ID ADL16947 standard; protein; 792 AA.  
DE Human NOVY protein homologue SeqID 483.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 72; DB 5; Length 792;  
Best Local Similarity 19.1%; Pred. No. 2e+02;  
RESULT 943  
ID ADD46435 standard; protein; 1106 AA.  
DE Rat Protein O63258, SEQ ID NO 12115.  
PN WO2003016475-A2.

PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 6.5%; Score 72; DB 7; Length 1106;  
Best Local Similarity 22.6%; Pred. No. 3.1e+02;  
RESULT 944  
ID ADN22331 standard; protein; 1447 AA.  
DE Bacterial polypeptide #4984.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CNOY/) CNO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.5%; Score 72; DB 8; Length 1447;  
Best Local Similarity 25.0%; Pred. No. 4.6e+02;  
RESULT 945  
ID ABU48947 standard; protein; 5005 AA.  
DE Protein encoded by Prokaryotic essential gene #34474.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.5%; Score 72; DB 6; Length 5005;  
Best Local Similarity 24.0%; Pred. No. 2.6e+03;  
RESULT 946  
ID ABP68524 standard; protein; 300 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:207.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 300;  
Best Local Similarity 24.6%; Pred. No. 57;  
RESULT 947  
ID ABP68461 standard; protein; 300 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:65.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 300;  
Best Local Similarity 24.6%; Pred. No. 57;  
RESULT 948  
ID ADM18942 standard; protein; 300 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:207.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 300;  
Best Local Similarity 24.6%; Pred. No. 57;  
RESULT 949  
ID ADM18700 standard; protein; 300 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:65.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 300;  
Best Local Similarity 24.6%; Pred. No. 57;  
RESULT 950  
ID ABP68462 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:66.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 951  
ID ABP68519 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:202.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;

RESULT 952  
ID ABP6854 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:217.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 953  
ID ABP68498 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:181.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 954  
ID ABP68463 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:67.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 955  
ID ABP68459 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:63.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 956  
ID ABP68504 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:187.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 957  
ID ABP68506 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:189.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 958  
ID ABP68526 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:209.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 959  
ID ABP68451 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:55.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 960  
ID ABP68454 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:58.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 961  
ID ABP68496 standard; protein; 303 AA.

ID ABP68456 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:60.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 962  
ID ABP68453 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:57.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 963  
ID ABP68448 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:52.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 964  
ID ABP68447 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:51.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 965  
ID ABP68511 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:194.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 966  
ID ABP68522 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:205.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 967  
ID ABP68525 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:208.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 968  
ID ABP68452 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:56.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 969  
ID ABP68450 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:54.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 970  
ID ABP68496 standard; protein; 303 AA.

DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:179.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 971  
ID ADM18614 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:179.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 972  
ID ADM18629 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:194.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 973  
ID ADM18701 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:66.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 974  
ID ADM18624 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:189.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 975  
ID ADM18616 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:181.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 976  
ID ADM18640 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:205.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 977  
ID ADM18698 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:63.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 978  
ID ADM18644 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:209.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 979  
ID ADM18693 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:58.

PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 980  
ID ADM18702 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:67.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 981  
ID ADM18637 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:202.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 982  
ID ADM18687 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:52.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 983  
ID ADM18643 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:208.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 984  
ID ADM18690 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:55.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 985  
ID ADM18686 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:51.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 986  
ID ADM18689 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:54.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 987  
ID ADM18691 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:56.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 988  
ID ADM18692 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:57.  
PN WO2004029197-A2.

PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 989  
ID ADM18822 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:187.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 990  
ID ADM18695 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:60.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 991  
ID ADM18852 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:217.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 58;  
RESULT 992  
ID ABB47969 standard; protein; 331 AA.  
DE Listeria monocytogenes protein #673.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTERUR.  
Query Match 6.5%; Score 71.5; DB 5; Length 331;  
Best Local Similarity 22.1%; Pred. No. 66;  
RESULT 993  
ID AAB88327 standard; protein; 348 AA.  
DE Human membrane or secretory protein clone PSEC0028.  
PN EPI067182-A2.  
PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.5%; Score 71.5; DB 4; Length 348;  
Best Local Similarity 21.7%; Pred. No. 71;  
RESULT 994  
ID ABB50797 standard; protein; 397 AA.  
DE Helicobacter pylori selected interacting domain (SID) protein #140.  
PN WO200265501-A2.  
PD 29-AUG-2002.  
PA (HYAR-) HYBRIGENICS.  
PA (INSP-) INST PASTERUR.  
Query Match 6.5%; Score 71.5; DB 5; Length 397;  
Best Local Similarity 18.7%; Pred. No. 85;  
RESULT 995  
ID ADP99057 standard; protein; 450 AA.  
DE C. albicans specific gene, orf19.3956, protein sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 6.5%; Score 71.5; DB 8; Length 450;  
Best Local Similarity 27.6%; Pred. No. 1e+02;  
RESULT 996  
ID AAY36758 standard; protein; 453 AA.  
DE Chlamydia trachomatis transport protein.  
PN WO9928475-A2.  
PD 10-JUN-1999.  
PA (GSEST-) GENSEST.  
Query Match 6.5%; Score 71.5; DB 2; Length 453;  
Best Local Similarity 24.6%; Pred. No. 1e+02;  
RESULT 997  
ID AAW77233 standard; protein; 508 AA.  
DE MiniMUC1 protein.

PN WO9837095-A2.  
PD 27-AUG-1998.  
PA (THER-) THERION BIOLOGICS CORP.  
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND-) DANA FARBER CANCER INST INC.  
Query Match 6.5%; Score 71.5; DB 2; Length 508;  
Best Local Similarity 23.1%; Pred. No. 1.2e+02;  
RESULT 998  
ID AAM41006 standard; protein; 522 AA.  
DE Human polypeptide SEQ ID NO 5937.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 71.5; DB 4; Length 522;  
Best Local Similarity 21.8%; Pred. No. 1.2e+02;  
RESULT 999  
ID AAG63982 standard; protein; 549 AA.  
DE Amino acid sequence of murine necrin-3.  
PN WO200166736-A1.  
PD 13-SEP-2001.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA (TAKA/) TAKAHASHI K.  
Query Match 6.5%; Score 71.5; DB 4; Length 549;  
Best Local Similarity 25.3%; Pred. No. 1.3e+02;  
RESULT 1000  
ID AAG63985 standard; protein; 549 AA.  
DE Amino acid sequence of murine necrin-3.  
PN WO200166736-A1.  
PD 13-SEP-2001.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA (TAKA/) TAKAHASHI K.  
Query Match 6.5%; Score 71.5; DB 4; Length 549;  
Best Local Similarity 25.3%; Pred. No. 1.3e+02;  
RESULT 1001  
ID AAB32391 standard; protein; 549 AA.  
DE Mouse necrin-3alpha protein.  
PN WO200228902-A2.  
PD 11-APR-2002.  
PA (IMMV-) IMMUNEX CORP.  
Query Match 6.5%; Score 71.5; DB 5; Length 549;  
Best Local Similarity 25.3%; Pred. No. 1.3e+02;  
RESULT 1002  
ID ABB64085 standard; protein; 559 AA.  
DE Human diagnostic and therapeutic protein SEQ ID NO:4334.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.5%; Score 71.5; DB 8; Length 559;  
Best Local Similarity 30.6%; Pred. No. 1.4e+02;  
RESULT 1003  
ID AAG30391 standard; protein; 668 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36324.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
PA (AAG30391) AAG30391 INC.  
Query Match 6.5%; Score 71.5; DB 3; Length 668;  
Best Local Similarity 24.7%; Pred. No. 1.8e+02;  
RESULT 1004  
ID AAG30390 standard; protein; 692 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36323.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
PA (AAG30390) AAG30390 INC.  
Query Match 6.5%; Score 71.5; DB 3; Length 692;  
Best Local Similarity 24.7%; Pred. No. 1.8e+02;  
RESULT 1005  
ID ABB93188 standard; protein; 692 AA.  
DE Hericidially active polypeptide SEQ ID NO 2399.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 6.5%; Score 71.5; DB 5; Length 692;  
Best Local Similarity 24.7%; Pred. No. 1.8e+02;  
RESULT 1006  
ID ABB58214 standard; protein; 713 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 1434.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.5%; Score 71.5; DB 4; Length 713;  
Best Local Similarity 24.5%; Pred. No. 1.9e+02;  
RESULT 1007  
ID ABR93899 standard; protein; 718 AA.  
DE Hebically active polypeptide SEQ ID NO 3110.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.5%; Score 71.5; DB 5; Length 718;  
Best Local Similarity 23.0%; Pred. No. 1.9e+02;  
RESULT 1008  
ID AAR49731 standard; protein; 796 AA.  
DE Sequence encoded by human OSF-4-1 cDNA.  
PN EP583801-A2.  
PD 09-MAR-1994.  
PA (FARH ) HOECHST JAPAN LTD.  
Query Match 6.5%; Score 71.5; DB 2; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1009  
ID AAW25636 standard; protein; 796 AA.  
DE Human cadherin-11.  
PN US5646250-A.  
PD 08-JUL-1997.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 6.5%; Score 71.5; DB 2; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1010  
ID AAW13334 standard; protein; 796 AA.  
DE Full length human cadherin-11.  
PN US5597725-A.  
PD 28-JAN-1997.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 6.5%; Score 71.5; DB 2; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1011  
ID AAW85598 standard; protein; 796 AA.  
DE Cadherin-11.  
PN WO9849560-A1.  
PD 05-NOV-1998.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match 6.5%; Score 71.5; DB 2; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1012  
ID AAB60419 standard; protein; 796 AA.  
DE Human PTP-binding protein, OB-cadherin-1 (cadherin-11).  
PN WO200100235-A1.  
PD 04-JAN-2001.  
PA (UYMC-) UNIV MCGILL.  
Query Match 6.5%; Score 71.5; DB 4; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1013  
ID AAB67624 standard; protein; 796 AA.  
DE Amino acid sequence of a human cadherin-11 polypeptide.  
PN WO200117557-A1.  
PD 15-MAR-2001.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 6.5%; Score 71.5; DB 4; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1014  
ID AD116950 standard; protein; 796 AA.  
DE Human NOVX protein homologue SeqID 486.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 71.5; DB 5; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1015  
ID ADP18662 standard; protein; 796 AA.

DE Human protein encoded by TAT400 cDNA used to treat cancer SeqID 22.  
PN WO2004045516-A2.  
PD 03-JUN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.5%; Score 71.5; DB 8; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1016  
ID ADP26903 standard; protein; 796 AA.  
DE Human OB-cadherin protein SEQ ID NO:4.  
PN EPI428893-A2.  
PD 16-JUN-2004.  
PA (SPRE/) SPRECHER E.  
Query Match 6.5%; Score 71.5; DB 8; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1017  
ID ADP48218 standard; protein; 796 AA.  
DE Human cadherin 11 type 2 OB-cadherin protein SEQ:6.  
PN WO2004074510-A1.  
PD 02-SEP-2004.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 6.5%; Score 71.5; DB 8; Length 796;  
Best Local Similarity 30.6%; Pred. No. 2.2e+02;  
RESULT 1018  
ID ABU30775 standard; protein; 936 AA.  
DE Protein encoded by Prokaryotic essential gene #16302.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.5%; Score 71.5; DB 6; Length 936;  
Best Local Similarity 18.7%; Pred. No. 2.8e+02;  
RESULT 1019  
ID ADN23173 standard; protein; 1139 AA.  
DE Bacterial polypeptide #5826.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.5%; Score 71.5; DB 8; Length 1139;  
Best Local Similarity 23.0%; Pred. No. 3.7e+02;  
RESULT 1020  
ID ABR33413 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1766.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 71; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.99;  
RESULT 1021  
ID ABR33283 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1636.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 71; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.99;  
RESULT 1022  
ID ABR33430 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1783.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 71; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.99;  
RESULT 1023  
ID ABR33422 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1775.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.

Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1024				
ID ABR333424 standard; peptide; 15 AA.				
DE Human cancer-related protein 156P5C12 HLA peptide #1777.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1025				
ID ABR333118 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1366.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1026				
ID ABR33116 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1364.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1027				
ID ABR33337 standard; peptide; 15 AA.				
DE Human cancer-related protein 156P5C12 HLA peptide #1680.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1028				
ID ABR33331 standard; peptide; 15 AA.				
DE Human cancer-related protein 156P5C12 HLA peptide #1684.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1029				
ID ABR33141 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1359.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1030				
ID ABR33429 standard; peptide; 15 AA.				
DE Human cancer-related protein 156P5C12 HLA peptide #1782.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1031				
ID ABR33348 standard; peptide; 15 AA.				
DE Human cancer-related protein 156P5C12 HLA peptide #1701.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1032				
ID ABR33124 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1342.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1033				
ID ABR33124 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1342.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1034				
ID ABR33124 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1342.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1035				
ID ABR33124 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1342.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match	6.4%;	Score 71;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	0.99;	
RESULT 1036				
ID ABR33124 standard; peptide; 15 AA.				
DE Human cancer-related protein 156PID4 HLA peptide #1342.				
PN WO200283921-A2.				
PD 24-OCT-2002.				
PA (AGEN-) AGENSYS INC.				
Query Match				

Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1033			
ID ABR33365 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P5C12 HLA peptide #1718.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1034			
ID ABR33304 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P1D4 HLA peptide #1322.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1035			
ID ABR33345 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P5C12 HLA peptide #1798.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1036			
ID ABR33402 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P5C12 HLA peptide #1755.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1037			
ID ABR33386 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P5C12 HLA peptide #1739.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1038			
ID ABR33093 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P1D4 HLA peptide #1311.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1039			
ID ABR33343 standard; peptide; 15 AA.			
DE Human cancer-related protein 156P5C12 HLA peptide #1696.			
PN WO200283921-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1040			
ID AAG09853 standard; protein; 81 AA.			
DE Argininosuccinate lyase protein fragment SEQ ID NO: 7946.			
PN EPI033405-A2.			
PD 06-SEP-2000.			
PA (AGEN-) AGENSYS INC.			
Query Match	6.4%;	Score 71; DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 0.99;	
RESULT 1041			
ID ABB69646 standard; protein; 183 AA.			
DE Human polypeptide SEQ ID NO: 1693.			
PN WO200270539-A2.			
PD 12-SEP-2002.			
PA (HYSE-) HYSEQ INC.			
Query Match	6.4%;	Score 71; DB 3;	Length 81;
Best Local Similarity	27.9%;	Pred. No. 10;	
RESULT 1042			
ID ABB69646 standard; protein; 183 AA.			
DE Human polypeptide SEQ ID NO: 1693.			
PN WO200270539-A2.			
PD 12-SEP-2002.			
PA (HYSE-) HYSEQ INC.			
Query Match	6.4%;	Score 71; DB 5;	Length 183;
Best Local Similarity	22.0%;	Pred. No. 33;	
RESULT 1042			

ID ADA55095 standard; protein: 183 AA.  
DE Human protein, SEQ ID 2663.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
DE (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 6; Length 183;  
RESULT 1043  
ID ADS74327 standard; protein: 183 AA.  
DE PRO polypeptide PRO92173, role in immune-related disease.  
PN WO2004081199-A2.  
PD 23-SEP-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 8; Length 183;  
RESULT 1044  
ID ABG15265 standard; protein: 234 AA.  
DE Novel human diagnostic protein #15256.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 4; Length 234;  
RESULT 1045  
ID ABR08196 standard; protein: 235 AA.  
DE DPCR1 gene product within human leukocyte antigen (HLA) domain.  
PN WO200248348-A1.  
PD 20-JUN-2002.  
PA (INOK) INOKO H.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 5; Length 235;  
RESULT 1046  
ID ADA84039 standard; protein: 235 AA.  
DE Human DPCR1 protein.  
PN WO2002103028-A2.  
PD 27-DEC-2002.  
PA (BIOM-) BIOMEDICAL CENT.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 6; Length 235;  
RESULT 1047  
ID ADN39108 standard; protein: 235 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:426.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 7; Length 235;  
RESULT 1048  
ID ADN39978 standard; protein: 235 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C348.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 7; Length 235;  
RESULT 1049  
ID ADN39977 standard; protein: 235 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C347.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 7; Length 235;  
RESULT 1050  
ID ADH18898 standard; protein: 330 AA.  
DE Human cell adhesion and extracellular matrix CADPCM-25 protein - SEQ 25.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 8; Length 330;  
RESULT 1051

ID ADO57299 standard; protein: 336 AA.  
DE Kidney development associated protein seqid 66.  
PN US2004068763-A1.  
PD 08-APR-2004.  
PA (HOPK) HOPKINS N.  
DE (GOLL) GOLING G.  
PA (AMST) AMSTERDAM A.  
PA (SUNZ) SUN Z.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 8; Length 336;  
RESULT 1052  
ID ABU04649 standard; protein: 338 AA.  
DE Human expressed protein tag (EPT) #1315.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 6; Length 338;  
RESULT 1053  
ID ABU04605 standard; protein: 338 AA.  
DE Human expressed protein tag (EPT) #1271.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 6; Length 338;  
RESULT 1054  
ID AAR20816 standard; protein: 361 AA.  
DE Haematopoietic CD44 antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GCHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 2; Length 361;  
RESULT 1055  
ID AAR9144 standard; protein: 361 AA.  
DE Human haematopoietic CD44 antigen.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GCHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 2; Length 361;  
RESULT 1056  
ID AAW80453 standard; protein: 361 AA.  
DE Human CD44 antigen (membrane form).  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GCHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 2; Length 361;  
RESULT 1057  
ID AAW86200 standard; protein: 361 AA.  
DE Human CD44 antigen (membrane form).  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GCHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 2; Length 361;  
RESULT 1058  
ID AAY99851 standard; protein: 361 AA.  
DE Human CD44 cell surface adhesion receptor.  
PN WO200035935-A1.  
PD 22-JUN-2000.  
PA (ISIS-) ISIS PHARM INC.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 3; Length 361;  
RESULT 1059  
ID AAY96139 standard; protein: 361 AA.  
DE Human haematopoietic CD44.5.  
PN US611093-A.  
PD 29-AUG-2000.  
PA (GCHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 6.4%; Score 71; DB 3; Length 361;



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Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1060
ID AB002448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GENO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 4; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1061
ID AB004622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1062
ID AB004632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1063
ID AB004643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1064
ID AB004610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1065
ID AB004638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1066
ID AB004634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1067
ID AB004626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1068
ID AB004630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1069
ID AB004609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1070
ID AB004644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1071
ID AB004607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1072
ID AB004636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1073
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1074
ID ADD90592 standard; protein; 361 AA.
DE Human CD44 glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 6.4%; Score 71; DB 7; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1075
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFER L.
PA (OQUE/) OQUENDO C.
PA (SIMW/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGLIN S.
PA (AMIO/) AMIOT M.
Query Match 6.4%; Score 71; DB 8; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1076
ID AD039385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 361;
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Best Local Similarity 20.2%; Pred. No. 84;  
RESULT 1077  
ID ABU04615 standard; protein; 395 AA.  
DE Human expressed protein tag (EPT) #1281.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 395;  
Best Local Similarity 20.2%; Pred. No. 96;  
RESULT 1078  
ID AD039389 standard; protein; 395 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.4%; Score 71; DB 8; Length 395;  
Best Local Similarity 20.2%; Pred. No. 96;  
RESULT 1079  
ID ABU04617 standard; protein; 425 AA.  
DE Human expressed protein tag (EPT) #1283.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 425;  
Best Local Similarity 20.2%; Pred. No. 1.1e+02;  
RESULT 1080  
ID AD039382 standard; protein; 425 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.4%; Score 71; DB 8; Length 425;  
Best Local Similarity 20.2%; Pred. No. 1.1e+02;  
RESULT 1081  
ID ABU04651 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1317.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 470;  
Best Local Similarity 20.2%; Pred. No. 1.2e+02;  
RESULT 1082  
ID ABU04603 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1269.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 470;  
Best Local Similarity 20.2%; Pred. No. 1.2e+02;  
RESULT 1083  
ID ABB49430 standard; protein; 489 AA.  
DE Listeria monocytogenes protein #2334.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match 6.4%; Score 71; DB 5; Length 489;  
Best Local Similarity 20.0%; Pred. No. 1.3e+02;  
RESULT 1084  
ID AAR20817 standard; protein; 493 AA.  
DE Epithelial CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 2; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1085  
ID AAR91445 standard; protein; 493 AA.  
DE Human epithelial CD44 antigen.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 2; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;

RESULT 1086  
ID AAW80454 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 2; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1087  
ID AAW89151 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 2; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1088  
ID AAY96140 standard; protein; 493 AA.  
DE Human epithelial CD44.  
PN US611093-A.  
PD 29-AUG-2000.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 3; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1089  
ID AAU02449 standard; protein; 493 AA.  
DE Human epithelial antigen CD44 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 4; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1090  
ID AAU99123 standard; protein; 493 AA.  
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.  
PN WO200244342-A2.  
PD 06-JUN-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 6.4%; Score 71; DB 5; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1091  
ID ABU04637 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1303.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1092  
ID ABU04627 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1293.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1093  
ID ABU04639 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1305.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1094  
ID ABU04623 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1289.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 493;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1095

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ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1096
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1097
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1098
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1099
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1100
ID ADJ93507 standard; protein; 493 AA.
DE Human CD4 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1101
ID ADO49375 standard; protein; 493 AA.
DE Human CD4 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALIE/) ALLEN J.
PA (ARUF/) ARUFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFER L.
PA (OQUE/) OQUEBDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMTO/) AMIOT M.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1102
ID ADO39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUN-2004.
PA (APPL-) APPLERA CORP.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.3e+02; Length 493;
RESULT 1103
ID ABB52510 standard; protein; 496 AA.
DE Escherichia coli polypeptide SEQ ID NO 370.
PN WO20016572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match
  Best Local Similarity 24.6%; Pred. No. 1.3e+02; Length 496;
RESULT 1104
ID ABU04961 standard; protein; 496 AA.
DE Protein encoded by Prokaryotic essential gene #26488.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
  Best Local Similarity 23.1%; Pred. No. 1.3e+02; Length 496;
RESULT 1105
ID AAM39220 standard; protein; 511 AA.
DE Human polypeptide SEQ ID NO 2365.
PN WO200153312-A1.
PD 26-JUN-2001.
PA (HYSE-) HYSEQ INC.
Query Match
  Best Local Similarity 21.1%; Pred. No. 1.4e+02; Length 511;
RESULT 1106
ID ADE95616 standard; protein; 514 AA.
DE Human NOVX28a protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match
  Best Local Similarity 23.0%; Pred. No. 1.4e+02; Length 514;
RESULT 1107
ID ABM63594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.5e+02; Length 535;
RESULT 1108
ID ADO39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUN-2004.
PA (APPL-) APPLERA CORP.
Query Match
  Best Local Similarity 20.2%; Pred. No. 1.5e+02; Length 535;
RESULT 1109
ID ADF06579 standard; protein; 542 AA.
DE Bacterial polypeptide #2692.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
  Best Local Similarity 23.1%; Pred. No. 1.5e+02; Length 542;
RESULT 1110
ID AAM35382 standard; protein; 560 AA.
DE Murine metacastic nucleic acid sequence product.
PN WO9718454-A2.
PD 22-MAY-1997.
PA (THOM/) THOMPSON T.
Query Match
  Best Local Similarity 23.0%; Pred. No. 1.6e+02; Length 560;
RESULT 1111
ID AAB11329 standard; protein; 560 AA.
DE Human lung cancer-associated protein L5285.
PN WO200061612-A2.
PD 19-OCT-2000.
PA (CORI-) CORIAX CORP.
Query Match
  Best Local Similarity 23.0%; Pred. No. 1.6e+02; Length 560;
RESULT 1112
ID ABB78200 standard; protein; 560 AA.
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DE Amino acid sequence of human HGFIN.  
PN WO200262947-A2.  
PA (UNNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
Query Match 6.4%; Score 71; DB 5; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1113  
ID ABB74961 standard; protein; 560 AA.  
DE Human lung tumour L528S protein sequence SEQ ID NO:225.  
PN WO200200174-A2.  
PD 03-JUN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 6.4%; Score 71; DB 5; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1114  
ID ABP61881 standard; protein; 560 AA.  
DE Human lung cancer associated protein sequence SEQ ID NO:225.  
PN WO200247534-A2.  
PD 20-JUN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 6.4%; Score 71; DB 5; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1115  
ID ABU56592 standard; protein; 560 AA.  
DE Lung cancer-associated polypeptide #185.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.4%; Score 71; DB 6; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1116  
ID ABG72962 standard; protein; 560 AA.  
DE Human osteocalcin homologue, nmb.  
PN US2002151486-A1.  
PD 17-OCT-2002.  
PA (POPO/) POPOFF S N.  
PA (SAFA/) SAFADI F F.  
PA (OWEN/) OWEN T A.  
PA (SMOC/) SMOCK S L.  
Query Match 6.4%; Score 71; DB 6; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1117  
ID ABU70852 standard; protein; 560 AA.  
DE Human adipocyte Selected Interacting domain, SID, #483.  
PN WO200286122-A2.  
PD 31-OCT-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 6.4%; Score 71; DB 6; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1118  
ID ADA28315 standard; protein; 560 AA.  
DE Human lung tumour L528S protein.  
PN US2003064947-A1.  
PD 03-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 6.4%; Score 71; DB 7; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1119  
ID ADP56520 standard; protein; 560 AA.  
DE Human NOVX28c protein.  
PN WO2003050245-A2.  
PD 19-JUN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.4%; Score 71; DB 7; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1120  
ID ADH36879 standard; protein; 560 AA.  
DE Human lung cancer-related protein #16.  
PN WO2003086175-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 6.4%; Score 71; DB 7; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;

RESULT 1121  
ID ADJ68660 standard; protein; 560 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID466.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 6.4%; Score 71; DB 7; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1122  
ID ADL14995 standard; protein; 560 AA.  
DE Human NMB protein for cancer treatment.  
PN WO2003068268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Query Match 6.4%; Score 71; DB 7; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1123  
ID ADN39940 standard; protein; 560 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C310.  
PN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.4%; Score 71; DB 7; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1124  
ID ADH56342 standard; protein; 560 AA.  
DE Human nmb protein SEQ ID NO:1.  
PN WO2004002516-A1.  
PD 08-JAN-2004.  
PA (TAKE ) TAKEIDA CHEM IND LTD.  
Query Match 6.4%; Score 71; DB 8; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1125  
ID ADJ75569 standard; protein; 560 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:821.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 6.4%; Score 71; DB 8; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1126  
ID ADM56682 standard; protein; 560 AA.  
DE Human lung tumour polypeptide #16.  
PN US2003138438-A1.  
PD 24-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 6.4%; Score 71; DB 8; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1127  
ID ADQ18310 standard; protein; 560 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1128.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.4%; Score 71; DB 8; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1128  
ID ADP23127 standard; protein; 560 AA.  
DE PRO polypeptide SEQ ID NO:221.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 560;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1129  
ID ADP66659 standard; protein; 563 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 171 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.

[illegible]

ID	ABJ72248	standard; protein; 572 AA.
DE	Human PRO9925 protein.	
PN	US2003050448-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 6; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1138		
ID	ABJ72376	standard; protein; 572 AA.
DE	Human PRO9925 protein.	
PN	US2003027988-A1.	
PD	06-FEB-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 6; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1140		
ID	ABJ72078	standard; protein; 572 AA.
DE	Human membrane bound receptor/protein PRO9925 amino acid sequence.	
PN	US2003065147-A1.	
PD	03-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 7; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1141		
ID	ADB89353	standard; protein; 572 AA.
DE	Novel human secreted and transmembrane protein PRO9925.	
PN	US2003073814-A1.	
PD	17-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 7; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1142		
ID	ADB89638	standard; protein; 572 AA.
DE	Novel human secreted and transmembrane protein PRO9925.	
PN	US2003088068-A1.	
PD	08-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 7; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1143		
ID	ADB7179	standard; protein; 572 AA.
DE	Novel human secreted and transmembrane protein PRO9925.	
PN	US2003093668-A1.	
PD	22-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 7; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1144		
ID	ADB78261	standard; protein; 572 AA.
DE	Novel human secreted and transmembrane protein PRO9925.	
PN	US2003092889-A1.	
PD	15-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 7; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1145		
ID	ADB84909	standard; protein; 572 AA.
DE	Human PRO polypeptide #21.	
PN	US2003073817-A1.	
PD	17-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	6.4%; Score 71; DB 7; Length 572;	
Best Local Similarity	23.0%; Pred. No. 1.6e+02;	
RESULT 1146		
ID	ADB78015	standard; protein; 572 AA.

DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1147  
ID ADB87081 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1148  
ID ADB84663 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1149  
ID ADB83778 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1150  
ID ADB72933 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1151  
ID ADC36771 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1152  
ID ADC21761 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1153  
ID ADD49792 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1154  
ID ADC48991 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1155  
ID ADD49508 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.

PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1156  
ID ADC47369 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1157  
ID ADC47114 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003105286-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1158  
ID ADC77989 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1159  
ID ADD06224 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1160  
ID ADC77743 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1161  
ID ADD50706 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1162  
ID ADD50952 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1163  
ID ADD50433 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1164  
ID ADD50187 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003096970-A1.

PD 22-MAY-2003  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1165  
ID ADE05198 atandard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1166  
ID ADB78235 standard; protein; 572 AA.  
DE Human CGDD-16.  
PN WO2003077875-A2.  
PD 25-SEP-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.4%; Score 71; DB 7; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1167  
ID ADC48745 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1168  
ID ADE05916 atandard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1169  
ID ADE05760 atandard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1170  
ID ADD74989 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1171  
ID ADD75735 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1172  
ID ADE04967 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1173  
ID ADB6793 atandard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1174  
ID ADE0670 atandard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1175  
ID ADE38967 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1176  
ID ADE05514 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1177  
ID ADD73499 atandard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1178  
ID ADB78339 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1179  
ID ADE21162 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1180  
ID ADD77277 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1181  
ID ADE20424 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1182  
ID ADB75489 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.





RESULT 1201  
ID ADG05555 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1202  
ID ADG27109 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1203  
ID ADG11172 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1204  
ID ADG11951 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1205  
ID ADP94508 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1206  
ID ADG06604 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1207  
ID ADH38948 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1208  
ID ADG34038 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1209  
ID ADI33508 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1210

ID ADH69602 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1211  
ID ADI29763 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1212  
ID ADM27160 standard; protein; 572 AA.  
DE Novel human secreted and transmembrane protein PRO9925.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1213  
ID ADK66518 standard; protein; 572 AA.  
DE Human PRO polypeptide #21.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 572;  
Best Local Similarity 23.0%; Pred. No. 1.6e+02;  
RESULT 1214  
ID ABB91918 standard; protein; 627 AA.  
DE Heridically active polypeptide SEQ ID NO 1129.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 6.4%; Score 71; DB 5; Length 627;  
Best Local Similarity 24.7%; Pred. No. 1.8e+02;  
RESULT 1215  
ID ABU04619 standard; protein; 668 AA.  
DE Human expressed protein tag (EPT) #1285.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 668;  
Best Local Similarity 20.2%; Pred. No. 2e+02;  
RESULT 1216  
ID ADQ39384 standard; protein; 668 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.4%; Score 71; DB 8; Length 668;  
Best Local Similarity 20.2%; Pred. No. 2e+02;  
RESULT 1217  
ID ABU04602 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1268.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 676;  
Best Local Similarity 20.2%; Pred. No. 2e+02;  
RESULT 1218  
ID ABU04652 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1318.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 676;  
Best Local Similarity 20.2%; Pred. No. 2e+02;  
RESULT 1219  
ID ABU24176 standard; protein; 685 AA.

DE Protein encoded by Prokaryotic essential gene #9703.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 6.4%; Score 71; DB 6; Length 685;  
Best Local Similarity 27.8%; Pred. No. 2.1e+02;  
RESULT 1220  
ID AAY81806 standard; protein; 686 AA.  
DE Human mahogany protein sequence #1.  
PN WO200005373-A2.  
PD 03-FEB-2000.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.4%; Score 71; DB 3; Length 686;  
Best Local Similarity 19.1%; Pred. No. 2.1e+02;  
RESULT 1221  
ID ABU04621 standard; protein; 691 AA.  
DE Human expressed protein tag (EPT) #1287.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 691;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1222  
ID AUQ39390 standard; protein; 691 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.4%; Score 71; DB 8; Length 691;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1223  
ID ABUS6470 standard; protein; 699 AA.  
DE Lung cancer-associated polypeptide #63.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.4%; Score 71; DB 6; Length 699;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1224  
ID ABU04647 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1313.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 699;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1225  
ID ABU04614 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1280.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 699;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1226  
ID ABU04608 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1274.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 699;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1227  
ID ADD90596 standard; protein; 699 AA.  
DE Human CD44v glycoprotein SEQ ID NO:6.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 6.4%; Score 71; DB 7; Length 699;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1228  
ID AAY97579 standard; protein; 700 AA.

DE Human CD44 splice variant (RA-CD44) protein sequence.  
PN WO200075312-A1.  
PD 14-DEC-2000.  
PA (YISS ) YISSUM RES & DEV CO.  
Query Match 6.4%; Score 71; DB 4; Length 700;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1229  
ID ABU04640 standard; protein; 700 AA.  
DE Human expressed protein tag (EPT) #1306.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 700;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1230  
ID ADD90594 standard; protein; 700 AA.  
DE Human CD44v glycoprotein SEQ ID NO:4.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 6.4%; Score 71; DB 7; Length 700;  
Best Local Similarity 20.2%; Pred. No. 2.1e+02;  
RESULT 1231  
ID ABU04604 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1270.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 719;  
Best Local Similarity 20.2%; Pred. No. 2.2e+02;  
RESULT 1232  
ID ABU04650 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1316.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 719;  
Best Local Similarity 20.2%; Pred. No. 2.2e+02;  
RESULT 1233  
ID ABG17071 standard; protein; 742 AA.  
DE Novel human diagnostic protein #17062.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 71; DB 4; Length 742;  
Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
RESULT 1234  
ID ABU04653 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1319.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 742;  
Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
RESULT 1235  
ID ABU04620 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1286.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 742;  
Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
RESULT 1236  
ID ABU04645 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1311.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.4%; Score 71; DB 6; Length 742;  
Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
RESULT 1237  
ID ABU04616 standard; protein; 742 AA.

DE Human expressed protein tag (EPT) #1282.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOs INC.  
 Query Match 6.4%; Score 71; DB 6; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1238  
 ID ADN95511 standard; protein; 742 AA.  
 DE Human BRC/LEC-related protein sequence SeqID434.  
 PN WO2003080640-A1.  
 PD 02-OCT-2003.  
 PA (LUDM-) LUDMIG INST CANCER RES.  
 PA (LICN-) LICENTIA LTD.  
 Query Match 6.4%; Score 71; DB 7; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1239  
 ID ADP65295 standard; protein; 742 AA.  
 DE Human CD44 antigen (homing function and Indian blood group system), CD44.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 6.4%; Score 71; DB 7; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1240  
 ID ADL61252 standard; protein; 742 AA.  
 DE Human protein tyrosine kinase biomarker CD44 antigen protein.  
 PN WO2004020583-A2.  
 PD 11-MAR-2004.  
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1241  
 ID ADI93506 standard; protein; 742 AA.  
 DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.  
 PN WO2004024750-A2.  
 PD 25-MAR-2004.  
 PA (DYMX-) DYMX CORP.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1242  
 ID ADOS5181 standard; protein; 742 AA.  
 DE Protein #83 with increased gene expression in renal cell carcinoma.  
 PN WO2004032842-A2.  
 PD 22-APR-2004.  
 PA (VAND-) VAN ANDEL INST.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1243  
 ID ADQ39383 standard; protein; 742 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1244  
 ID ADQ39391 standard; protein; 742 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1245  
 ID ADQ39386 standard; protein; 742 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1246  
 ID ADR67253 standard; protein; 742 AA.

DE Human bladder cancer associated amino acid sequence.  
 PN WO2004076613-A2.  
 PD 10-SEP-2004.  
 PA (HERR-) HERR A.  
 PA (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (STAUF/) STAUB E.  
 PA (PILA/) PILARSKY C.  
 PA (SPEC/) SPECCH T.  
 Query Match 6.4%; Score 71; DB 8; Length 742;  
 Best Local Similarity 20.2%; Pred. No. 2.3e+02;  
 RESULT 1247  
 ID AAU09864 standard; protein; 801 AA.  
 DE Novel human secreted protein #5.  
 PN WO200179454-A1.  
 PD 25-OCT-2001.  
 PA (SMIK-) SMITHKLINE BEECHAM CORP.  
 PA (SMIK-) SMITHKLINE BEECHAM PLC.  
 Query Match 6.4%; Score 71; DB 5; Length 801;  
 Best Local Similarity 31.8%; Pred. No. 2.6e+02;  
 RESULT 1248  
 ID ADU70665 standard; protein; 801 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID2471.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 6.4%; Score 71; DB 7; Length 801;  
 Best Local Similarity 31.8%; Pred. No. 2.6e+02;  
 RESULT 1249  
 ID AAE02339 standard; protein; 873 AA.  
 DE Drosophila melanogaster chloride channel (dmcLC) protein.  
 PN WO200138359-A2.  
 PD 31-MAY-2001.  
 PA (GENO-) GENOPTERA LLC.  
 Query Match 6.4%; Score 71; DB 4; Length 873;  
 Best Local Similarity 20.9%; Pred. No. 2.9e+02;  
 RESULT 1250  
 ID ADJ83142 standard; protein; 1161 AA.  
 DE Murine integrin alpha 7 protein - SEQ ID 133.  
 PN US2003170630-A1.  
 PD 11-SEP-2003.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (TCHE/) TCHERNEV V T.  
 PA (LITUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (PATY/) PATYURAJAN M.  
 PA (LEPL/) LEPLLEY D M.  
 PA (BURG/) BURGESS C E.  
 PA (SHIM/) SHIMKETS R A.  
 PA (GROS/) GROSSE W M.  
 PA (SZER/) SZEKERES E S.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (CASM/) CASMAN S J.  
 PA (BOLD/) BOLDOS F L.  
 PA (GORM/) GORMAN L.  
 PA (GANG/) GANGOLI E A.  
 PA (FERN/) FERNANDES E R.  
 PA (RIEG/) RIEGER D K.  
 PA (EDIN/) EDINGER S R.  
 PA (GUNT/) GUNTHER B.  
 PA (MILL/) MILLER T.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MACD/) MACDOUGALL J R.  
 PA (SMIT/) SMITHSON G.  
 Query Match 6.4%; Score 71; DB 7; Length 1161;  
 Best Local Similarity 22.3%; Pred. No. 4.3e+02;  
 RESULT 1251  
 ID ADL6198 standard; protein; 1238 AA.  
 DE Mouse protein tyrosine phosphatase #4.

PN W02003068984-A2.  
 PD 21-AUG-2003.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1238;  
 RESULT 1252  
 ID AAY70690 standard; protein: 1355 AA.  
 DE Human membrane attractin-1.  
 PN W0200015651-A1.  
 PD 23-MAR-2000.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 3; Length 1355;  
 RESULT 1253  
 ID ADI21666 standard; protein: 1370 AA.  
 DE Novel human polypeptide #145.  
 PN W02003025148-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1370;  
 RESULT 1254  
 ID AAY70691 standard; protein: 1429 AA.  
 DE Human membrane attractin-2.  
 PN W0200015651-A1.  
 PD 23-MAR-2000.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 3; Length 1429;  
 RESULT 1255  
 ID ABG08472 standard; protein: 1429 AA.  
 DE Novel human diagnostic protein #8463.  
 PN W0200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 4; Length 1429;  
 RESULT 1256  
 ID AND39110 standard; protein: 1460 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:428.  
 PN W02003042861-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1460;  
 RESULT 1257  
 ID ABB57380 standard; protein: 1495 AA.  
 DE Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 12.  
 PN W0200183705-A1.  
 PD 08-NOV-2001.  
 PA (KXOM) KYOMA HAKKO KOGYO KK.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 5; Length 1495;  
 RESULT 1258  
 ID ADB57115 standard; protein: 1496 AA.  
 DE Rat Protein L19180, SEQ ID NO 2975.  
 PN W02003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1496;  
 RESULT 1259  
 ID ADB57119 standard; protein: 1496 AA.  
 DE Rat Protein L19180, SEQ ID NO 2979.  
 PN W02003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1496;  
 RESULT 1260

ID ADD47013 standard; protein: 1496 AA.  
 DE Rat Protein L19180, SEQ ID NO 12699.  
 PN W02003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1496;  
 RESULT 1261  
 ID ADD47017 standard; protein: 1496 AA.  
 DE Rat Protein L19180, SEQ ID NO 12703.  
 PN W02003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1496;  
 RESULT 1262  
 ID AAR72858 standard; protein: 1501 AA.  
 DE Rat receptor type-protein tyrosine phosphatase sigma.  
 PN W09509656-A1.  
 PD 13-APR-1995.  
 PA (UTNY) UNIV NEW YORK STATE.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 2; Length 1501;  
 RESULT 1263  
 ID ADI21202 standard; protein: 1538 AA.  
 DE Novel human protein #177.  
 PN W02003025148-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1538;  
 RESULT 1264  
 ID ADD46989 standard; protein: 1863 AA.  
 DE Rat Protein AAC37656, SEQ ID NO 12675.  
 PN W02003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 7; Length 1863;  
 RESULT 1265  
 ID ABB57100 standard; protein: 1904 AA.  
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:224.  
 PN W0200188188-A2.  
 PD 22-NOV-2001.  
 PA (UTNY) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 5; Length 1904;  
 RESULT 1266  
 ID AAR71726 standard; protein: 1911 AA.  
 DE Human PTP-OB.  
 PN W09507935-A1.  
 PD 23-MAR-1995.  
 PA (MERI) MERCK & CO INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 2; Length 1911;  
 RESULT 1267  
 ID AAW27225 standard; protein: 1911 AA.  
 DE Human protein tyrosine phosphatase PTP-OB.  
 PN US5658756-A.  
 PD 19-AUG-1997.  
 PA (MERI) MERCK & CO INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 2; Length 1911;  
 RESULT 1268  
 ID AAW94027 standard; protein: 1911 AA.  
 DE Human protein tyrosine phosphatase (PTP-OB).  
 PN US5866397-A.  
 PD 02-FEB-1999.  
 PA (MERI) MERCK & CO INC.  
 Query Match  
 Best Local Similarity 6.4%; Score 71; DB 2; Length 1911;

Best Local Similarity 31.8%; Pred. No. 8.7e+02;  
RESUR 1269  
ID AAU01459 standard; protein; 1911 AA.  
DE Human protein cytosine phosphatase, PRP-OB, amino acid sequence.  
PN US6214564-B1.  
PD 10-APR-2001.  
PA (MERI) MERCK & CO INC.  
Query Match 6.4%; Score 71; DB 4; Length 1911;  
Best Local Similarity 31.8%; Pred. No. 8.7e+02;  
RESUR 1270  
ID ADD18742 standard; protein; 1948 AA.  
DE Human disease related protein Segid173.  
PN WO2003018621-A2.  
PD 06-MAR-2003  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 6.4%; Score 71; DB 7; Length 1948;  
Best Local Similarity 31.8%; Pred. No. 8.9e+02;  
RESUR 1271  
ID ADE57117 standard; protein; 1949 AA.  
DE Human Protein U35234, SEQ ID NO 2977.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 7; Length 1949;  
Best Local Similarity 31.8%; Pred. No. 8.9e+02;  
RESUR 1272  
ID ADE57121 standard; protein; 1949 AA.  
DE Human Protein U35234, SEQ ID NO 2981.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 7; Length 1949;  
Best Local Similarity 31.8%; Pred. No. 8.9e+02;  
RESUR 1273  
ID ADD47019 standard; protein; 1949 AA.  
DE Human Protein U35234, SEQ ID NO 12705.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 7; Length 1949;  
Best Local Similarity 31.8%; Pred. No. 8.9e+02;  
RESUR 1274  
ID ADD47015 standard; protein; 1949 AA.  
DE Human Protein U35234, SEQ ID NO 12701.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 71; DB 7; Length 1949;  
Best Local Similarity 31.8%; Pred. No. 8.9e+02;  
RESUR 1275  
ID ADP3496 standard; protein; 2000 AA.  
DE PRO polypeptide SEQ ID NO:674.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GEHT) GENENTECH INC.  
Query Match 6.4%; Score 71; DB 8; Length 2000;  
Best Local Similarity 25.6%; Pred. No. 9.3e+02;  
RESUR 1276  
ID AA81807 standard; protein; 2787 AA.  
DE Human mahogany protein sequence #2.  
PN WO200005373-A2.  
PD 03-FEB-2000.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.4%; Score 71; DB 3; Length 2787;  
Best Local Similarity 19.1%; Pred. No. 1.5e+03;  
RESUR 1277  
ID ADN7315 standard; protein; 5155 AA.  
DE Thale cress protein upregulated in E2pa/Dpa expressing plants Segid 1040.  
PN WO2004035798-A2.

PD 29-APR-2004.  
PA (CROP-) CROPPESIGN NV.  
Query Match 6.4%; Score 71; DB 8; Length 5155;  
Best Local Similarity 18.4%; Pred. No. 3.5e+03;  
RESUR 1278  
ID AAM38777 standard; protein; 138 AA.  
DE Human polypeptide SEQ ID NO 1922.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 4; Length 138;  
Best Local Similarity 22.3%; Pred. No. 25;  
RESUR 1279  
ID AAU14339 standard; protein; 138 AA.  
DE Human novel protein #210.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 4; Length 138;  
Best Local Similarity 22.3%; Pred. No. 25;  
RESUR 1280  
ID AAM40563 standard; protein; 155 AA.  
DE Human polypeptide SEQ ID NO 5494.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 4; Length 155;  
Best Local Similarity 22.3%; Pred. No. 29;  
RESUR 1281  
ID ABB90250 standard; protein; 258 AA.  
DE Human polypeptide SEQ ID NO 2626.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.4%; Score 70.5; DB 5; Length 258;  
Best Local Similarity 24.9%; Pred. No. 60;  
RESUR 1282  
ID ABB68491 standard; protein; 303 AA.  
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:174.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.4%; Score 70.5; DB 5; Length 303;  
Best Local Similarity 24.6%; Pred. No. 75;  
RESUR 1283  
ID ADM18809 standard; protein; 303 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:174.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.4%; Score 70.5; DB 8; Length 303;  
Best Local Similarity 24.6%; Pred. No. 75;  
RESUR 1284  
ID ADR41425 standard; protein; 305 AA.  
DE Human CD-like molecule HOUCD83, SEQ ID NO:224.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.4%; Score 70.5; DB 5; Length 305;  
Best Local Similarity 24.9%; Pred. No. 76;  
RESUR 1285  
ID AAY9188 standard; protein; 516 AA.  
DE Soybean cytochrome P450 enzyme, CYP83D1.  
PN WO9919493-A2.  
PD 22-APR-1999.  
PA (UNYC-) UNIV NORTH CAROLINA STATE.  
Query Match 6.4%; Score 70.5; DB 2; Length 516;  
Best Local Similarity 23.2%; Pred. No. 1.6e+02;  
RESUR 1286  
ID ABB58504 standard; protein; 518 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2304.  
PN WO200171042-A2.  
PD 27-SEP-2001.

PA (PEKE ) PE CORP NY.  
Query Match 6.4%; Score 70.5; DB 4; Length 518;  
Best Local Similarity 24.2%; Pred. No. 1.6e+02;  
RESULT 1287  
ID AAM39143 standard; protein; 555 AA.  
DE Human polypeptide SEQ ID NO 2288.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 4; Length 555;  
Best Local Similarity 24.9%; Pred. No. 1.8e+02;  
RESULT 1288  
ID ABP69054 standard; protein; 801 AA.  
DE Human polypeptide SEQ ID NO 1101.  
PN WO200270639-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 5; Length 801;  
Best Local Similarity 32.0%; Pred. No. 2.9e+02;  
RESULT 1289  
ID AAY72616 standard; protein; 854 AA.  
DE Carassius auratus full-length CaSR-like protein #3.  
PN WO200105833-A1.  
PD 23-JAN-2001.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 6.4%; Score 70.5; DB 4; Length 854;  
Best Local Similarity 27.5%; Pred. No. 3.2e+02;  
RESULT 1290  
ID ABB93062 standard; protein; 900 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2273.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.4%; Score 70.5; DB 5; Length 900;  
Best Local Similarity 26.4%; Pred. No. 3.4e+02;  
RESULT 1291  
ID ABG21347 standard; protein; 1131 AA.  
DE Novel human diagnostic protein #21338.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 4; Length 1131;  
Best Local Similarity 22.0%; Pred. No. 4.7e+02;  
RESULT 1292  
ID ABG24027 standard; protein; 1142 AA.  
DE Novel human diagnostic protein #24018.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70.5; DB 4; Length 1142;  
Best Local Similarity 22.0%; Pred. No. 4.8e+02;  
RESULT 1293  
ID ABB71304 standard; protein; 1171 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40704.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.4%; Score 70.5; DB 4; Length 1171;  
Best Local Similarity 18.5%; Pred. No. 5e+02;  
RESULT 1294  
ID ADS43524 standard; protein; 1173 AA.  
DE Bacterial polypeptide #21954.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HTNK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.4%; Score 70.5; DB 8; Length 1173;  
Best Local Similarity 20.1%; Pred. No. 5e+02;  
RESULT 1295  
ID AAY07729 standard; protein; 1183 AA.

DE Armenian hamster alpha-2 integrin subunit protein.  
PN WO9916465-A1.  
PD 08-APR-1999.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (SENG/) SENGHER D R.  
PA (DETM/) DETMAR M.  
PA (CLAF/) CLAFFEY K P.  
Query Match 6.4%; Score 70.5; DB 2; Length 1183;  
Best Local Similarity 23.5%; Pred. No. 5e+02;  
RESULT 1296  
ID ABR52622 standard; protein; 2000 AA.  
DE Protein sequence #SEQ ID 109.  
PN EPI258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 6.4%; Score 70.5; DB 6; Length 2000;  
Best Local Similarity 21.6%; Pred. No. 1.1e+03;  
RESULT 1297  
ID ADR62602 standard; protein; 2000 AA.  
DE Disease treating protein complex-derived protein #427.  
PN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 6.4%; Score 70.5; DB 7; Length 2000;  
Best Local Similarity 21.6%; Pred. No. 1.1e+03;  
RESULT 1298  
ID ABR33444 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1797.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 70; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
RESULT 1299  
ID ABR33416 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1769.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 70; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
RESULT 1300  
ID ABR3322 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1675.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 70; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
RESULT 1301  
ID ABR33294 standard; peptide; 15 AA.  
DE Human cancer-related protein 156P5C12 HLA peptide #1647.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.4%; Score 70; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
RESULT 1302  
ID AAG74274 standard; protein; 176 AA.  
DE Human colon cancer antigen protein SEQ ID NO:5038.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMANA GENOME SCI INC.  
Query Match 6.4%; Score 70; DB 4; Length 176;  
Best Local Similarity 22.1%; Pred. No. 40;  
RESULT 1303  
ID ABR64767 standard; protein; 216 AA.  
DE Human protein SEQ ID 427.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70; DB 5; Length 216;  
Best Local Similarity 19.3%; Pred. No. 53;

RESULT 1304  
ID ABU1212 standard; protein; 221 AA.  
DE Protein encoded by Prokaryotic essential gene #26739.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA) PHARM INC.  
Query Match 6.4%; Score 70; DB 6; Length 221;  
Best Local Similarity 28.3%; Pred. No. 55;  
RESULT 1305  
ID ADQ59457 standard; protein; 298 AA.  
DE Human cancer-associated (CA) protein sequence SEQ ID NO:93.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 6.4%; Score 70; DB 8; Length 298;  
Best Local Similarity 19.5%; Pred. No. 83;  
RESULT 1306  
ID ABP29640 standard; protein; 341 AA.  
DE Streptococcus polypeptide SEQ ID NO 8456.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.4%; Score 70; DB 5; Length 341;  
Best Local Similarity 26.1%; Pred. No. 1e+02;  
RESULT 1307  
ID ABU46900 standard; protein; 341 AA.  
DE Protein encoded by Prokaryotic essential gene #32427.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA) PHARM INC.  
Query Match 6.4%; Score 70; DB 6; Length 341;  
Best Local Similarity 26.1%; Pred. No. 1e+02;  
RESULT 1308  
ID ADQ65785 standard; protein; 396 AA.  
DE Novel human protein sequence #758.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.4%; Score 70; DB 8; Length 396;  
Best Local Similarity 23.5%; Pred. No. 1.2e+02;  
RESULT 1309  
ID ABB54978 standard; protein; 544 AA.  
DE Lactococcus lactis protein uxbB.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.4%; Score 70; DB 5; Length 544;  
Best Local Similarity 25.7%; Pred. No. 1.9e+02;  
RESULT 1310  
ID ABB08976 standard; protein; 563 AA.  
DE Novel human diagnostic protein #8967.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.4%; Score 70; DB 4; Length 563;  
Best Local Similarity 20.8%; Pred. No. 2e+02;  
RESULT 1311  
ID ABB65057 standard; protein; 678 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21963.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.4%; Score 70; DB 4; Length 678;  
Best Local Similarity 24.6%; Pred. No. 2.6e+02;  
RESULT 1312  
ID ABB58451 standard; protein; 738 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2145.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.4%; Score 70; DB 4; Length 738;  
Best Local Similarity 22.3%; Pred. No. 3e+02;

RESULT 1313  
ID AAU38924 standard; protein; 738 AA.  
DE Drosophila G-protein coupled receptor, GCPR #2.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.4%; Score 70; DB 4; Length 738;  
Best Local Similarity 22.3%; Pred. No. 3e+02;  
RESULT 1314  
ID ADC35754 standard; protein; 738 AA.  
DE Drosophila G protein coupled receptor seq id 4.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 6.4%; Score 70; DB 7; Length 738;  
Best Local Similarity 22.3%; Pred. No. 3e+02;  
RESULT 1315  
ID ADN96168 standard; protein; 863 AA.  
DE Human NOVX polypeptide #111.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON/) ZHONG M.  
PA (LIDL/) LI L.  
PA (GORM/) GORMAN L.  
PA (SPYT/) SPYTEK K A.  
PA (KEKU/) KEKUDA R.  
PA (TAUP/) TAUPIER R J.  
PA (ANDE/) ANDERSON D W.  
PA (VERN/) VERNET C A M.  
PA (CATT/) CATTERTON E.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (TCHN/) TCHERNEV V T.  
PA (PADI/) PADIGARU M.  
PA (GUSE/) GUSEV V Y.  
PA (MALY/) MALYANKAR U M.  
PA (BURG/) BURGESS C E.  
PA (GERL/) GERLACH V.  
PA (CASM/) CASMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.  
PA (ROTH/) ROTHENBERG M E.  
PA (LARO/) LAROCHELLE W J.  
PA (SHIM/) SHIMKETS R A.  
PA (CRAB/) CRABTREE J.  
PA (RAST/) RASTELLI L.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDIG F L.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLER I.  
PA (MACD/) MACDOUGALL J R.  
PA (ELER/) ELLERMAN K.  
PA (CHAP/) CHAPOVAL A.  
Query Match 6.4%; Score 70; DB 8; Length 863;  
Best Local Similarity 22.9%; Pred. No. 3.7e+02;  
RESULT 1316  
ID AAY49554 standard; protein; 1039 AA.  
DE Human platelet membrane glycoprotein IIb protein sequence.  
PN WO950454-A2.  
PD 07-OCT-1999.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 6.4%; Score 70; DB 2; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1317  
ID AAY92445 standard; protein; 1039 AA.  
DE Wild type human GpIIb, form Bak-a.  
PN WO200020634-A1.  
PD 13-APR-2000.

PA (NOVA-) NOVA MOLECULAR INC.  
Query Match 6.4%; Score 70; DB 3; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1318  
ID AAY92446 standard; protein; 1039 AA.  
DE Variant human GPIIb, form Bak-b.  
PN WO200020634-A1.  
PD 13-APR-2000.  
PA (NOVA-) NOVA MOLECULAR INC.  
Query Match 6.4%; Score 70; DB 3; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1319  
ID ADD45808 standard; protein; 1039 AA.  
DE Human Protein P08514, SEQ ID NO 11477.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 6.4%; Score 70; DB 7; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1320  
ID ADB60212 standard; protein; 1039 AA.  
DE Human Protein P08514, SEQ ID NO 6118.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 6.4%; Score 70; DB 7; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1321  
ID AD122190 standard; protein; 1039 AA.  
DE Human platelet membrane glycoprotein IIb protein SEQ.153.  
PN WO2004005890-A2.  
PD 15-JAN-2004.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 6.4%; Score 70; DB 8; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1322  
ID ADM99591 standard; protein; 1039 AA.  
DE Human integrin alphaIIb subunit precursor protein.  
PN WO2004007530-A2.  
PD 22-JAN-2004.  
PA (BLCO-) CENT BLOOD RES INC.  
Query Match 6.4%; Score 70; DB 8; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1323  
ID ADP12420 standard; protein; 1039 AA.  
DE Protein encoded by mRNA of the invention #30.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 6.4%; Score 70; DB 8; Length 1039;  
Best Local Similarity 20.2%; Pred. No. 4.8e+02;  
RESULT 1324  
ID ADP74025 standard; protein; 1178 AA.  
DE Murine CD49b protein, a target of Th1 helper T cells Seq 15.  
PN JP2004147534-A.  
PD 27-MAY-2004.  
PA (NISH/) NISHIMURA T.  
PA (TORA ) TORAY IND INC.  
Query Match 6.4%; Score 70; DB 8; Length 1178;  
Best Local Similarity 23.8%; Pred. No. 5.7e+02;  
RESULT 1325  
ID ABG30775 standard; protein; 214 AA.  
DE Human vesicular membrane-spanning protein VIP36-23.54.  
PN CN1341651-A.  
PD 27-MAR-2002.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 6.3%; Score 69.5; DB 5; Length 214;  
Best Local Similarity 21.7%; Pred. No. 60;  
RESULT 1326  
ID ADR09157 standard; protein; 215 AA.  
DE Human protein useful for treating neurological disease Seq 2663.

PN EPI447413-A2.  
ID 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.3%; Score 69.5; DB 8; Length 215;  
Best Local Similarity 24.7%; Pred. No. 60;  
RESULT 1327  
ID AAU75545 standard; protein; 270 AA.  
DE Mouse B7-like protein, B7-L\_m2.  
PN WO200200710-A2.  
PD 03-JAN-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 6.3%; Score 69.5; DB 5; Length 270;  
Best Local Similarity 24.4%; Pred. No. 83;  
RESULT 1328  
ID ADJ94243 standard; protein; 274 AA.  
DE Mouse IPC marker Ly-49Q, SEQ ID 2.  
PN WO2004013325-A1.  
PD 12-FEB-2004.  
PA (GINK-) GINKGO BIOMEDICAL RES INST CO LTD.  
Query Match 6.3%; Score 69.5; DB 8; Length 274;  
Best Local Similarity 25.3%; Pred. No. 84;  
RESULT 1329  
ID AAU03560 standard; protein; 290 AA.  
DE Mouse immunoregulatory protein B7-H1.  
PN WO200139722-A2.  
PD 07-JUN-2001.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 6.3%; Score 69.5; DB 4; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1330  
ID AAY72646 standard; protein; 290 AA.  
DE Murine B7-4 protein.  
PN WO200114556-A1.  
PD 01-MAR-2001.  
PA (DAND ) DNA FARMER CANCER INST INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1331  
ID AAY72678 standard; protein; 290 AA.  
DE Murine B7-4 protein.  
PN WO200114557-A1.  
PD 01-MAR-2001.  
PA (DAND ) DNA FARMER CANCER INST INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1332  
ID AAB16963 standard; protein; 290 AA.  
DE Mouse PD-1 ligand (PD-L1).  
PN WO200200730-A2.  
PD 03-JAN-2002.  
PA (GEVY ) GENETICS INST INC.  
Query Match 6.3%; Score 69.5; DB 5; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1333  
ID AA015819 standard; protein; 290 AA.  
DE Murine B7H1 protein.  
PN US2002106730-A1.  
PD 08-AUG-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.3%; Score 69.5; DB 5; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1334  
ID AAB33392 standard; protein; 290 AA.  
DE Murine B7-4 protein.  
PN WO200279499-A1.  
PD 10-OCT-2002.  
PA (AMMP ) WYETH.  
PA (DAND ) DNA FARMER CANCER INST INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1335



ID ABJ18520 standard; protein; 290 AA.  
DE Murine PD-L1 protein.  
PN WO200278731-A1.  
PD 10-OCT-2002.  
PA (AMMP) WYETH.  
Query Match 6.3%; Score 69.5; DB 6; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1336  
ID ABG75660 standard; protein; 290 AA.  
DE Murine PD-L1 polypeptide.  
PN US2002164600-A1.  
PD 07-NOV-2002.  
PA (FREEB) FREEMAN G.  
PA (CHER/) CHERNOVA T.  
PA (MALE/) MALENKOVICH N.  
PA (WOOD/) WOOD C.  
Query Match 6.3%; Score 69.5; DB 6; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1337  
ID ADJ76248 standard; protein; 290 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1500.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 6.3%; Score 69.5; DB 8; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1338  
ID ADQ76324 standard; protein; 290 AA.  
DE Murine B7-H1 protein.  
PN US2004137577-A1.  
PD 15-JUL-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.3%; Score 69.5; DB 8; Length 290;  
Best Local Similarity 23.6%; Pred. No. 91;  
RESULT 1339  
ID ABU01702 standard; protein; 296 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1278.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.3%; Score 69.5; DB 6; Length 296;  
Best Local Similarity 20.6%; Pred. No. 94;  
RESULT 1340  
ID ABU6086 standard; protein; 296 AA.  
DE Protein encoded by Prokaryotic essential gene #31613.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 296;  
Best Local Similarity 20.6%; Pred. No. 94;  
RESULT 1341  
ID ABP68464 standard; protein; 302 AA.  
DE Novel co-stimulatory molecule (NC5M) Protein SEQ ID NO:68.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.3%; Score 69.5; DB 5; Length 302;  
Best Local Similarity 21.0%; Pred. No. 97;  
RESULT 1342  
ID ADM18703 standard; protein; 302 AA.  
DE Human co-stimulatory molecule protein SEQ ID NO:68.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Query Match 6.3%; Score 69.5; DB 8; Length 302;  
Best Local Similarity 21.0%; Pred. No. 97;  
RESULT 1343  
ID AAM79020 standard; protein; 313 AA.  
DE Human protein SEQ ID NO 1682.  
PN WO200157190-A2.  
PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 313;  
Best Local Similarity 21.7%; Pred. No. 1e+02;  
RESULT 1344  
ID ABB12008 standard; peptide; 314 AA.  
DE Human PRO704 homologue, SEQ ID NO:2378.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 314;  
Best Local Similarity 21.7%; Pred. No. 1e+02;  
RESULT 1345  
ID AAM60004 standard; protein; 314 AA.  
DE Human protein SEQ ID NO 3650.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 314;  
Best Local Similarity 21.7%; Pred. No. 1e+02;  
RESULT 1346  
ID AAM67846 standard; protein; 323 AA.  
DE Human secreted protein encoded by gene 40 clone HTOEU03.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.3%; Score 69.5; DB 2; Length 323;  
Best Local Similarity 21.7%; Pred. No. 1.1e+02;  
RESULT 1347  
ID AAY41741 standard; protein; 348 AA.  
DE Human PRO704 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH-) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 2; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1348  
ID AAB44297 standard; protein; 348 AA.  
DE Human PRO704 (UNQ368) protein sequence SEQ ID NO:380.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH-) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 3; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1349  
ID AAB88578 standard; protein; 348 AA.  
DE Human hydrophobic domain containing protein clone HP03747 #62.  
PN WO200112660-A2.  
PD 22-FEB-2001.  
PA (SAGA) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1350  
ID AAU29070 standard; protein; 348 AA.  
DE Human PRO polypeptide sequence #47.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1351  
ID AAM39973 standard; protein; 348 AA.  
DE Human polypeptide SEQ ID NO 3118.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.3%; Score 69.5; DB 4; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1352  
ID ABU52863 standard; protein; 348 AA.  
DE Intracellular transport and trafficking protein from DKFpzhbr2\_23124.  
PN WO200112659-A2.  
PD 22-FEB-2001.

PA (GERH-) GERMAN HUMAN GENOME PROJECT.  
Query Match 6.3%; Score 69.5; DB 4; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1353  
ID ABB89148 standard; protein; 348 AA.  
DE Human polypeptide SEQ ID NO 1524.  
PN W0200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.3%; Score 69.5; DB 5; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1354  
ID ABUS8446 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1355  
ID ABUS7994 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1356  
ID ABUS4309 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1357  
ID ABR66183 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1358  
ID ABR65573 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1359  
ID ABUS9513 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1360  
ID ABUS2752 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1361  
ID ABUS9873 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1362  
ID ABR68122 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;

Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1363  
ID ABUS6175 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1364  
ID ABUS92606 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1365  
ID ABO08683 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1366  
ID ABO02735 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1367  
ID ABR74889 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1368  
ID ABR94651 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1369  
ID ABO25243 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1370  
ID ABUS6524 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GERH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1371  
ID ABUS98784 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003031353-A1.  
PD 16-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1372  
ID ABUS97999 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;

RESULT 1373  
ID ABU91705 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1374  
ID ABUT7249 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1375  
ID ABU8398 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1376  
ID ABU6239 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1377  
ID ABU67452 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1378  
ID ABU80480 standard; protein; 348 AA.  
DE Human PRO protein #47.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1379  
ID ABR9339 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1380  
ID ABR8788 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1381  
ID ABO16311 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1382  
ID ABR9221 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1383  
ID ABO1852 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1384  
ID ABR78273 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1385  
ID ABUS009 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1386  
ID ABO00148 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1387  
ID ABO11480 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1388  
ID ABO02125 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1389  
ID ABUS8699 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1390  
ID ABUS394 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1391  
ID ABO06195 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003022824-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1392  
ID ABR59231 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1393

Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1393  
ID ABO1852 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1394  
ID ABR78273 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1395  
ID ABUS009 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1396  
ID ABO00148 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1397  
ID ABO11480 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1398  
ID ABO02125 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1399  
ID ABUS8699 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1400  
ID ABUS394 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1401  
ID ABO06195 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003022824-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1402  
ID ABR59231 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 21.7%; Pred. No. 1.2e+02; Length 348;  
RESULT 1403

ID ABO09293 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1394  
ID ABO19157 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1395  
ID ABO11175 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1396  
ID ABR66793 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1397  
ID ABO16006 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1398  
ID ABO13712 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1399  
ID ABR84929 standard; protein; 348 AA.  
DE Human secreted and transmembrane PRO polypeptide #5.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1400  
ID ABR65615 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein, SEQ ID 94.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1401  
ID ABO07463 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1402  
ID ABO03650 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1403  
ID ABR67098 standard; protein; 348 AA.

DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1404  
ID ABO15701 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1405  
ID ABR55982 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein, PRO704.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1406  
ID ABR61127 standard; protein; 348 AA.  
DE Human PRO704 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1407  
ID ABR65310 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1408  
ID ABR95255 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1409  
ID ABR71158 standard; protein; 348 AA.  
DE Human PRO704 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1410  
ID ABO07768 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1411  
ID ABR70009 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1412  
ID ABR69342 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1413  
ID ABO01483 standard; protein; 348 AA.

DE Human PRO polypeptide #47.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1414  
ID ABU61285 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1415  
ID ABR60082 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1416  
ID ABR67817 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1417  
ID ABR65205 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1418  
ID ABR68427 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1419  
ID ABR71839 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1420  
ID ABR65319 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1421  
ID ABUS9009 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1422  
ID ABUS3089 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1423  
ID ABUS9495 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1424  
ID ABUS9493 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1425  
ID ABUS4004 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1426  
ID ABUS655 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1427  
ID ABR64900 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1428  
ID ABR68732 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1429  
ID ABO06548 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1430  
ID ABR99093 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1431  
ID ABUS6977 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1432  
ID ABUS5929 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1433  
ID ABUS2216 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003036136-A1.  
PD 20-FEB-2003.

Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1444			
ID ABR69096 standard; protein; 348 AA.			
DE Human secreted polypeptide PRO704, SEQ ID NO:94.			
PN US2003040058-A1.			
PD 27-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1445			
ID ABR94333 standard; protein; 348 AA.			
DE Human PRO polypeptide #47.			
PN US2003017540-A1.			
PD 23-JAN-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1446			
ID ABR79215 standard; protein; 348 AA.			
DE Human PRO polypeptide #47.			
PN US2003032106-A1.			
PD 13-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1447			
ID ABR8654 standard; protein; 348 AA.			
DE Human secreted/cranmembrane protein (PRO) #47.			
PN US2003032129-A1.			
PD 13-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1448			
ID ABR8649 standard; protein; 348 AA.			
DE Novel human secreted and transmembrane protein PRO704.			
PN US2003032131-A1.			
PD 13-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1449			
ID ABR94638 standard; protein; 348 AA.			
DE Human PRO polypeptide #47.			
PN US2003032103-A1.			
PD 13-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1450			
ID ABR04565 standard; protein; 348 AA.			
DE Human PRO polypeptide #47.			
PN US2003032107-A1.			
PD 13-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1451			
ID ABR70314 standard; protein; 348 AA.			
DE Human secreted polypeptide PRO704, SEQ ID NO:94.			
PN US2003032139-A1.			
PD 13-FEB-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1452			
ID ABR98479 standard; protein; 348 AA.			
DE Human PRO polypeptide #47.			
PN US2003022501-A1.			
PD 30-JAN-2003.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1453			
ID ABR65878 standard; protein; 348 AA.			
DE Human secreted polypeptide PRO704, SEQ ID NO:94.			
PN US2003036165-A1.			
PD 20-FEB-2003.			
PA (GENH ) GENENTECH INC.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	
RESULT 1454			
ID ABR65878 standard; protein; 348 AA.			
DE Human secreted polypeptide PRO704, SEQ ID NO:94.			
PN US2003036165-A1.			
PD 20-FEB-2003.			
PA (GENH ) GENENTECH INC.			
Query Match	6.3%;	Score 69.5; DB 6;	Length 348;
Best Local Similarity	21.7%;	Pred. No. 1.2e+02;	

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Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1475  
ID ABO04970 standard; protein; 348 AA.  
DE Novel human secreted and transmembrane protein PRO704.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1476  
ID ABO08378 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1477  
ID ABO05585 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1478  
ID ABR73974 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1479  
ID ABR5566 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1480  
ID ABR80863 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1481  
ID ABR81168 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1482  
ID ABO00864 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1483  
ID ABR88466 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1484  
ID ABR77287 standard; protein; 348 AA.

DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1485  
ID ABO28771 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1486  
ID ABO31516 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1487  
ID ABO07933 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1488  
ID ABO40413 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1489  
ID ABO35838 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1490  
ID ABO43977 standard; protein; 348 AA.  
DE Human PRO polypeptide #47.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1491  
ID ADA77846 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1492  
ID ABR24772 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1493  
ID ABO03040 standard; protein; 348 AA.  
DE Human secreted/transmembrane protein (PRO) #47.  
PN US2003036131-A1.



PD 20-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1494  
ID ABR90296 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1495  
ID ABM17210 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1496  
ID ABR94956 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1497  
ID ABR95261 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1498  
ID ABO21499 standard; protein; 348 AA.  
DE Human secreted/cranmembrane protein (PRO) #47.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1499  
ID ABR97763 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;  
RESULT 1500  
ID ABR87551 standard; protein; 348 AA.  
DE Human secreted polypeptide PRO704, SEQ ID NO:94.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.3%; Score 69.5; DB 6; Length 348;  
Best Local Similarity 21.7%; Pred. No. 1.2e+02;

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